



GGA TGG ACA GTC TAT GGT CTG GCA ACT CTC CTC ATC CTC ACA GTC ACA GCC ATT GTA GCA	1266
K I L L H V T F K S H R V P A S G D L R	431
AAG ATA CTT CTG CAC GTC ACA TTC AAA TCC CAT CGT GTT CCT GCT TCA GGG GAC CTT AGG	1326
D C H Q P G T S G E I W S I F Y K P S T	451
GAT TGT CAT CAA CCA GGG ACT TCG GGG GAA ATC TGG AGC ATT TTT TAC AAG CCT TCC ACT	1386
S I S I F K K K L K G Q S Q Q D D R N P	471
TCA ATT TCC ATC TTT AAG AAG AAA CTC AAG GGT CAG AGT CAA CAA GAT GAC CGC AAT CCC	1446
L V S D *	476
CTT GTG AGT GAC TAA	1461

AAACCCCACTGTGCCTAGGACTTGAGGTCCCTCTTTGAGCTCAAGGCTGCCGTGGTCAACCTCTCCTGTGGTTCTTCTC	1540
TGACAGACTCTTCCCTCCTCTCCCTCTGCCTCGGCCTCTTCGGGGAAACCCTCCTCCTACAGACTAGGAAGAGGCACC	1619
TGCTGCCAGGGCAGGCAGAGCCTGGATTTCCTCCTGCTT	1657

Fig. 1B

Fig. 1C

GTCGACCCACGCGTCCGCCCGGCTCCCGGTGCTGCCCCCTCTGCCCCGGGCGCGCCCGGGGTCCCGCACTGACGGCC 79  
 M A P P A A R L A L L S A A A L T L A 19  
 C ATG GCG CCG CCC GCC GCC CGT CTC GCG CTG CTC TCC GCC GCT GCG CTC ACT CTG GCG 137  
 A R P A P G P R S G P E C F T A N G A D 39  
 GCC CGG CCC GCG CCC GGT CCC CGC TCC GGC CCC GAG TGC TTC ACA GCC AAC GGT GCA GAT 197  
 Y R G T Q S W T A L Q G G K P C L F W N 59  
 TAC AGG GGA ACA CAG AGC TGG ACA GCG CTG CAA GGT GGG AAG CCA TGT CTG TTC TGG AAC 257  
 E T F Q H P Y N T L K Y P N G E G G L G 79  
 GAG ACT TTC CAG CAT CCG TAC AAC ACG CTG AAG TAC CCC AAC GGG GAA GGA GGA CTG GGC 317  
 E H N Y C R N P D G D V S P W C Y V A E 99  
 GAG CAC AAT TAT TGC AGA AAT CCA GAT GGA GAC GTG AGC CCT TGG TGC TAC GTG GCC GAG 377  
 H E D G V Y W K Y C E I P A C Q M P G N 119  
 CAT GAG GAC GGA GTC TAC TGG AAG TAC TGT GAA ATT CCT GCC TGC CAG ATG CCT GGA AAC 437  
 L G C Y K D H G N P P P L T G T S K T S 139  
 CTT GGC TGC TAC AAG GAT CAT GGA AAC CCA CCT CCT CTC ACG GGC ACC AGT AAA ACC TCT 497  
 N K L T I Q T C I S F C R S Q R F K F A 159  
 AAC AAG CTC ACC ATA CAA ACC TGT ATC AGC TTC TGT CGG AGT CAG AGA TTC AAG TTT GCT 557  
 G M E S G Y A C F C G N N P D Y W K H G 179  
 GCG ATG GAG TCA GGC TAT GCC TGC TTC TGT GGG AAC AAT CCT GAC TAC TGG AAG CAC GGG 617  
 E A A S T E C N S V C F G D H T Q P C G 199  
 GAG GCG GCC AGC ACC GAG TGC AAT AGT GTC TGC TTC GGG GAC CAC ACG CAG CCC TGC GGT 677  
 G D G R I I L F D T L V G A C G G N Y S 219  
 GGG GAC GGC AGG ATT ATC CTC TTT GAC ACT CTC GTG GGC GCC TGC GGT GGG AAC TAC TCA 737  
 A M A A V V Y S P D F P D T Y A T G R V 239  
 GCC ATG GCA GCC GTG GTG TAC TCC CCT GAC TTC CCT GAC ACC TAC GCC ACT GGC AGA GTC 797  
 C Y W T I R V P G A S R I H F N F T L F 259  
 TGC TAC TGG ACC ATC CGG GTT CCA GGA GCC TCT CGC ATC CAT TTC AAC TTC ACC CTG TTT 857  
 D I R D S A D M -V E L L D G Y T H R V L 279  
 GAT ATC AGG GAC TCT GCA GAC ATG GTG GAG CTG CTG GAC GGC TAC ACC CAC CGC GTC CTG 917  
 V R L S G R S R P P L S F N V S L D F V 299  
 GTC CGG CTC AGT GGG AGG AGC CGC CCG CCT CTG TCT TTC AAT GTC TCT CTG GAT TTT GTC 977  
 I L Y F F S D R I N Q A Q G F A V L Y Q 319  
 ATT TTG TAT TTC TTC TCT GAT CGC ATC AAT CAG GCC CAG GGA TTT GCT GTG TTG TAC CAA 1037  
 A T K E E P P Q E R P A V N Q T L A E V 339  
 GCC ACC AAG GAG GAA CCG CCA CAG GAG AGA CCT GCT GTC AAC CAG ACC CTG GCA GAG GTG 1097  
 I T E Q A N L S V S A A H S S K V L Y V 359

ATC ACC GAG CAA GCC AAC CTC AGT GTC AGC GCT GCC CAC TCC TCC AAA GTC CTC TAT GTC 1157  
 I T P S P S H P P Q T A Q V A I P G H R 379  
 ATC ACC CCC AGC CCC AGC CAC CCT CCG CAG ACT GCC CAG GTA GCC ATT CCT GGG CAC CGT 1217  
 Q L G P T A T E W K D G L C T A W R P S 399  
 CAG TTG GGG CCA ACA GCC ACA GAG TGG AAG GAT GGA CTG TGT ACG GCC TGG CGA CCC TCC 1277  
 S S S Q S Q Q L S Q R F F C M S H L N L 419  
 TCA TCC TCA CAG TCA CAG CAG TTG TCG CAA AGA TTC TTC TGC ATG TCA CAT TTA AAT CTC 1337  
 I E S L H Q E T L G T V V S L G L L E I 439  
 ATC GAG TCC CTG CAT CAG GAG ACC TTA GGG ACT GTC GTC AGC CTG GGG CTT CTG GAG ATA 1397  
 S G P F S M N L P L Q S P S L R R S S R 459  
 TCT GGA CCA TTT TCT ATG AAC CTT CCA CTA CAA TCT CCA TCT TTA AGA AGA AGC TCA AGG 1457  
 V R V N K M T A I P S \* 471  
 GTC AGA GTC AAC AAG ATG ACC GCA ATC CCC TCG TGA 1493  
 GTGACTGAAGCCCACGCCTGCATGAGAGGCTCCGCTCCAAGCTCGAGTTTGCTCCCCCTGAGTTCTCCTCTGATGAGTTC 1572  
 CCGCCCTTCCCATTACACCACCATCTCTTTTGGGAGCACCCCTGCTTTAGAGGCAGCCCAGCCTGGGATCCTCCATCACAT 1651  
 GTACCAGCCTGGCTGCTCTGCTGGGGATGGTAAGACAGGCCCAGGCTGACAGGACACAGCTGGACCTGACTCCAGAAGA 1730  
 CTCTTGGGTGGTGGGGAGGTATAGTGTAGGATGAGTTTTCTTGCTTCTTCTCTGTTTTGTCCACATACAGATCGGTTTC 1809  
 CCGTGTCTTTACAGTTTGCAATAGAGCCAGACTGAAAGAACTGTCAGGTTTTCTAGGCTGGCCTGGTTCCCCACTAAGA 1888  
 GTGGCATTGGCGCCCTAGAGGCCCAGAGGCCCAGTGTAGGCTTGGAGCTTTCTCTGCTGCCAACTACCATGTGTCATCT 1967  
 AGTCCGAGGGGACTGAGAGCAGGGCCACACCAGATGTCATCTTTCTAGAGGGTTCTTTTGTAGTACCCACTGACCAATGG 2046  
 GGCAAGCCTGAGGATTGGTCCATCTGTTTGTCCATGGAACAGACACAGTGAACCTCCTGGATACTAGACTTAACTAGCC 2125  
 TAGCCCTCAAGTAGTTGCCAATCCTGTGGAATCAGAATTCAGCCTGTCTTCTGTCTCAGCCCAAGCCTGTAGCCTAG 2204  
 AGCTGGGGCTGTAGCCTAGAGCTGGGGCTGTAGCCTAGAGCTGGGGCTGTAGCACAGAGCTGGGGCTGTAGCCTAGAGC 2283  
 TGGGGCTGTAGCACAGAGCTGGGGCTGTAGCCTAGAGCTGGGGCTGTAGCACAGAGCTGGGGCTGTAGCACAGAGCTGG 2362  
 GGCTGTAGCCTAGAGCTGGGGCTGTAGCACAGAGCTGGGGCTGTAACCTCAGCGATCAAGAGCTTGCTTTGTATACATCG 2441  
 GACCCTAGGTTCTATCCCAGCACTATCAGAAGGTGGGAGAGAAAAAGACTGCACCATAGCATGCGGGCAGCATCTGTGG 2520  
 TTCTTACGTGAGGTGTCATCATTTTAAAAGCAGATCAAACTACCGCGAGTTTGTTCCTTTGTCCCTTATCATGGGAGC 2599  
 AGAGTAGGAGTAAGGGCTCTGGTCTTGCTCATTTGTCCCCCAGACAGGGAGGCAGGAAAAGGTCAGGCTTGGGAACCTGGA 2678  
 GATCCTCCCAGGAAAAGCTGCAAGATTGAGAGACCCAGCTGCAGTTGGGAGAGGAAGGGCCATCCCCGACTGAGAAGTC 2757  
 CTGCAGTCTGGAAGTGGCCTTTGTGTCAGCAGCAGCTGTGCCCTGAAGGTAGACCTTGGTCACTCTCCTGCCAGCCCTTGA 2836  
 GCCTCTGCTCTCCTGGGTACCCTCCTGGAACACCATGCTAACCTTCCCCGAGTCTCTCAGTCACTGCCATTGAGGCCTC 2915  
 TCCTCTAGCTGCTGCTCCCCAGGACTGTCTGGGGCCATCTGGGGATCAGGGAGAGGCAGCAGGAGTACTGACGAGGCAG 2994

TGACCTGAGCTGATGAGTCAACCAGAGGACACCAGAGTCTACAGTGGGCTGGCTGCTGGCTCAGCTCCTATGGGAGGCC 3073  
 TACAGGGGTACTAAGCTAGGGGGTCATCATCTCATTTGATCTGGGAAAGGCTACAGGCTCCTGGATGTGAAGACAGGCC 3152  
 CACTACATAAGAAGACCACTGGAAATAGACTGACAGGAGCAGGTTCCACTCTAGGCTGTCCATAGCGTTTGCAGGACTC 3231  
 CCCTGAGACCAAGTGTGAGTACAGAGTGCCATGTGCGTAGTGCATAAAGGATATGGGTTCCTTAACCAGGGAAGGCTC 3310  
 ATAGCAGGCCAGGACATTTTTTCAGCTCAGAGCACTGGCCCCAGGCTTCCTCTAAGCCACCACCTCACCTGTCTCTTCCT 3389  
 ATCTCGGACACAGGAAGCAAGCCCCAGTGTGGTGGCAGCTGCGGCTCAGCATTGGTGTCCCCAGGAAGGGCGGTGGATG 3468  
 TGCCACGCTCCTTTTGCTGTGGGCCTGGCACAGCCCAACACTGCAGGGGCCACCTTCTCTCTTGGGGGGTAGGGACAC 3547  
 ATAAGGAAAACCTAACCCACCTCCAACAACAGCAGAGGACAGTGGGAAGGAAGGGCTGTAAATCACCCAGGCCAGACCTC 3626  
 CAGAAATGACAGGCACAGTCTGTTAGAACCTGTAGGCAGCCAGTCACAGAGGGCCCTTTGTGCTGGTAACACCCTGCCTG 3705  
 GAGCATAGGGGTAAAGCCGAGGGAGAAGAGCAGCCCTCAGAGACATCAGCTAAAAACATAGGTGCCCTATGTCCCTCCCT 3784  
 TCCTGTCACACTGCTTACAAAGCAGAGACAGAGTAGGAAAGAGGTCTTCATCCTCTCCCACATCAGCAAGGATAGGGCT 3863  
 GCGGCTGCCTAAAGTGAGCAAGGAGAACAGAGCTCTGGACTTCTCTAAATGTGGGCTCTGGCTTCAGACTCCTCAGCCA 3942  
 AAAGCTCTTGAAGATCAAAGCTCTGGCGGGTACAGCTGTCTGGCCTGTGGGCCAGCCCATGGGATGTGCCTGGGCCAG 4021  
 GTGCCACCCACGGCTCACTGTCTATCCAGGAGGGACCCACCTGATGCTCCTCATCATCCGCTGGCCTGACACTATCA 4100  
 GAGCTCGCGCCGGCTGTTGCCAGGGACAGACTGACTACACTTGACCTTCAAGAGCACTTAGAAGTGGATGGCCTCCAGA 4179  
 CTCGTGCAGCCTCTGCAGGGGCCACACAAGTCTCCCAGCCAAGTCCACAAGCCTCCATGGTTCCCTGGCTCCTCTCCT 4258  
 GTGGAGTGTCTGTTTGATGTCTGAGGTCTGCTTTGGGTACCGCCCTGGGAACCTGCTAACCTCCGATTGGTCCCTTTGT 4337  
 GTCTCTGTTTACTGTCTCTTCTACCTCCAGGTCACCTTAGCTCTGGCTGCTCTGGCTGGGAGTGGGGGGTGGGGATGCT 4416  
 GGTGTCACCCCAACCCTGGTCTGCCAACAGAACCTGGGGGGCTCACACGGGCTCCTGTCTTGCCAAGCTGGAGCTGAGC 4495  
 ACCTGGCCCAGGCTGAGTGGGGCAGAGCAAACAAGTGAAGGGGATCTCTCTCCTTAGAGGGAGGTGGCCGAAGGTGT 4574  
 AGATCCAGCGAGGGAGCTGCCATCCCCGCCACCTTCATAGCAGCAAGACCTTCCCATTTCCAATCTCACCTCCAGCAG 4653  
 GGATATGACTTTGGACAACAAGGCTTTATTTGTAAATATGCTCTTAATATGCAACTTTGAGAATAAGATAGAAACATCA 4732  
 TGTATTTTAAATATATAAAATGAAGTGTGACACACTGTATACAATTTAATATATATTTTTAGGATTTTGTATTTAAGAA 4811  
 AATGGAATGTGATGGTACTTAACTTTTACAAAAGAGAGAAAATGTTATTTTTACTGTTTGAAGAAAATAAATATTCTCA 4890  
 TTGTTGTAGAAAAAAGGGCGGCCGC 4928

Fig. 1E

	10	20	30	40	50	60	70
Hum.	MAPPAARLALLSAAALTLAARPAPSPGLGPGPECFTANGADYRGTQNTALQGGKPCLFWNETFQHPYNT						
Mur.	MAPPAARLALLSAAALTLAARPAPGPR--SGPECFTANGADYRGTQSWTALQGGKPCLFWNETFQHPYNT						
	10	20	30	40	50	60	
	80	90	100	110	120	130	140
Hum.	LKYPNGEGGLGEHNYCRNPDGDVSPWCYVAEHEDGVYWKYCEIPACQMPGNLGCYKDHGNNPPLTGTSTK						
Mur.	LKYPNGEGGLGEHNYCRNPDGDVSPWCYVAEHEDGVYWKYCEIPACQMPGNLGCYKDHGNNPPLTGTSTK						
	70	80	90	100	110	120	130
	150	160	170	180	190	200	210
Hum.	SNKLTITQTCISFCRSQRKFAGMESGYACFCGNNPDYWKYGEAASTECNSVCFGDHTQPCGGDGRILFD						
Mur.	SNKLTITQTCISFCRSQRKFAGMESGYACFCGNNPDYWKHGEAASTECNSVCFGDHTQPCGGDGRILFD						
	140	150	160	170	180	190	200
	220	230	240	250	260	270	280
Hum.	TLVGACGGNYSAMSSVVYSPDFPDYATGRVCYWTIRVPGASHIHFSFPLFDIRDSADMVELLDGYTHRV						
Mur.	TLVGACGGNYSAMAAVVYSPDFPDYATGRVCYWTIRVPGASRIHFNTLFDIRDSADMVELLDGYTHRV						
	210	220	230	240	250	260	270
	290	300	310	320	330	340	350
Hum.	LARFHGRSRPPLSFNVSLDFVILYFFSDRINQAQGFVLYQAVKEELPQERPAVNQTVAEVITEQANLSV						
Mur.	LVRLSGRSRPPLSFNVSLDFVILYFFSDRINQAQGFVLYQATKEEPPQERPAVNQTVAEVITEQANLSV						
	280	290	300	310	320	330	340
	360	370	380	390	400	410	420
Hum.	SAARSSKVLYVITTPSHPPQTVPGSNSWAPPMGAGSHRVEGWTVYGLATLLILTVAIVAKILLHVTFK						
Mur.	SAAHSSKVLYVITTPSHPPQTAQVAIPGHRQLGPTA---TEWKD-GLCTAWRPSSSSSQSQQLSQRFFCM						
	350	360	370	380	390	400	410
	430	440	450	460	470		
Hum.	SHRVPASGDLRDCHQPGTSGEIWSIFYKPSTISIFKKKLKGQSQ-QDDRNPLVSD						
Mur.	SHLNLIESLHQETLGTVVSLGLEISGPFSSMNLPLQSPSLRRSSRVVKNMTAIPS						
	420	430	440	450	460	470	

Fig. 1F

Fig. 1G

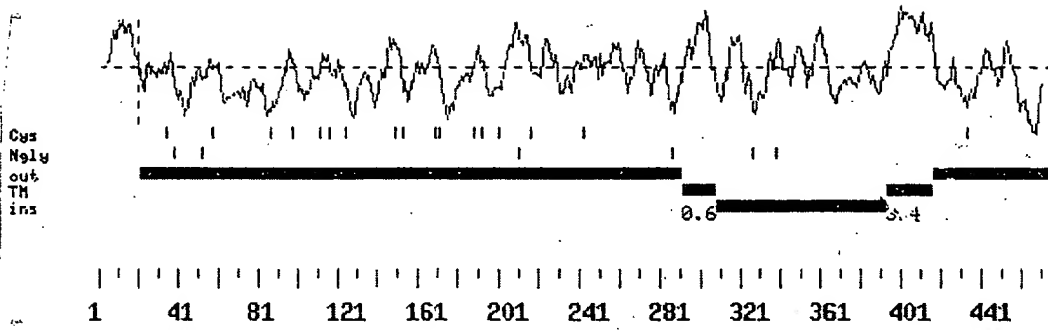


Fig. 1H

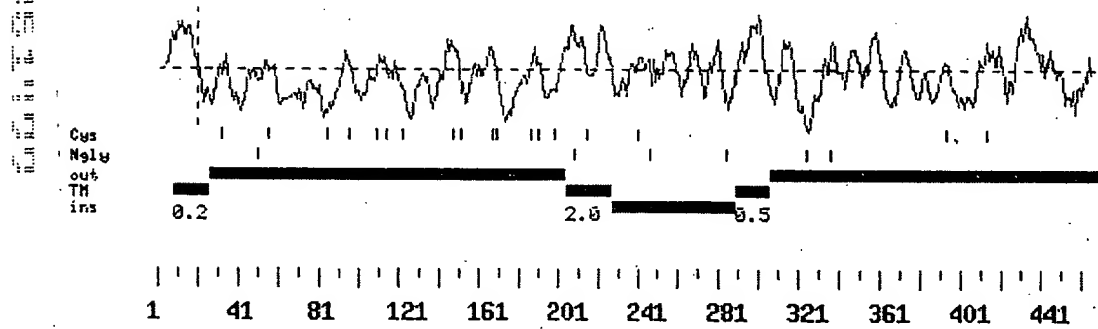


Fig. 2A

								M	M	L	P	Q	N	S	W	H	I	D	F	G	13
GCGGCCGCTCGCGATCTAGAACTAGTA	ATG	ATG	CTG	CCT	CAA	AAC	TCG	TGG	CAT	ATT	GAT	TTT	GGA								66
R	C	C	C	H	Q	N	L	F	S	A	V	V	T	C	I	L	L	L	N		33
AGA	TGC	TGC	TGT	CAT	CAG	AAC	CTT	TTC	TCT	GCT	GTG	GTA	ACT	TGC	ATC	CTG	CTC	CTG	AAT		126
S	C	F	L	I	S	S	F	N	G	T	D	L	E	L	R	L	V	N	G		53
TCC	TGC	TTT	CTC	ATC	AGC	AGT	TTT	AAT	GGA	ACA	GAT	TTG	GAG	TTG	AGG	CTG	GTC	AAT	GGA		186
D	G	P	C	S	G	T	V	E	V	K	F	Q	G	Q	W	G	T	V	C		73
GAC	GGT	CCC	TGC	TCT	GGG	ACA	GTG	GAG	GTG	AAA	TTC	CAG	GGA	CAG	TGG	GGG	ACT	GTG	TGT		246
D	D	G	W	N	T	T	A	S	T	V	V	C	K	Q	L	G	C	P	F		93
GAT	GAT	GGG	TGG	AAC	ACT	ACT	GCC	TCA	ACT	GTC	GTG	TGC	AAA	CAG	CTT	GGA	TGT	CCA	TTT		306
S	F	A	M	F	R	F	G	Q	A	V	T	R	H	G	K	I	W	L	D		113
TCT	TTC	GCC	ATG	TTT	CGT	TTT	GGA	CAA	GCC	GTG	ACT	AGA	CAT	GGA	AAA	ATT	TGG	CTT	GAT		366
D	V	S	C	Y	G	N	E	S	A	L	W	E	C	Q	H	R	E	W	G		133
GAT	GTT	TCC	TGT	TAT	GGA	AAT	GAG	TCA	GCT	CTC	TGG	GAA	TGT	CAA	CAC	CGG	GAA	TGG	GGA		426
S	H	N	C	Y	H	G	E	D	V	G	V	N	C	Y	G	E	A	N	L		153
AGC	CAT	AAC	TGT	TAT	CAT	GGA	GAA	GAT	GTT	GGT	GTG	AAC	TGT	TAT	GGT	GAA	GCC	AAT	CTG		486
G	L	R	L	V	D	G	N	N	S	C	S	G	R	V	E	V	K	F	Q		173
GGT	TTG	AGG	CTA	GTG	GAT	GGA	AAC	AAC	TCC	TGT	TCA	GGG	AGA	GTG	GAG	GTG	AAA	TTC	CAA		546
E	R	W	G	T	I	C	D	D	G	W	N	L	N	T	A	A	V	V	C		193
GAA	AGG	TGG	GGG	ACT	ATA	TGT	GAT	GAT	GGG	TGG	AAC	TTG	AAT	ACT	GCT	GCC	GTG	GTG	TGC		606
R	Q	L	G	C	P	S	S	F	I	S	S	G	V	V	N	S	P	A	V		213
AGG	CAA	CTA	GGA	TGT	CCA	TCT	TCT	TTT	ATT	TCT	TCT	GGA	GTT	GTT	AAT	AGC	CCT	GCT	GTA		666
L	R	P	I	W	L	D	D	I	L	C	Q	G	N	E	L	A	L	W	N		233
TTG	CGC	CCC	ATT	TGG	CTG	GAT	GAC	ATT	TTA	TGC	CAG	GGG	AAT	GAG	TTG	GCA	CTC	TGG	AAT		726
C	R	H	R	G	W	G	N	H	D	C	S	H	N	E	D	V	T	L	T		253
TGC	AGA	CAT	CGT	GGA	TGG	GGA	AAT	CAT	GAC	TGC	AGT	CAC	AAT	GAG	GAT	GTC	ACA	TTA	ACT		786
C	Y	D	S	S	D	L	E	L	R	L	V	G	G	T	N	R	C	M	G		273
TGT	TAT	GAT	AGT	AGT	GAT	CTT	GAA	CTA	AGG	CTT	GTA	GGT	GGA	ACT	AAC	CGC	TGT	ATG	GGG		846
R	V	E	L	K	I	Q	G	R	W	G	T	V	C	H	H	K	W	N	N		293
AGA	GTA	GAG	CTG	AAA	ATC	CAA	GGA	AGG	TGG	GGG	ACC	GTA	TGC	CAC	CAT	AAG	TGG	AAC	AAT		906
A	A	A	D	V	V	C	K	Q	L	G	C	G	T	A	L	H	F	A	G		313
GCT	GCA	GCT	GAT	GTC	GTA	TGC	AAG	CAG	TTG	GGA	TGT	GGA	ACC	GCA	CTT	CAC	TTC	GCT	GGC		966
L	P	H	L	Q	S	G	S	D	V	V	W	L	D	G	V	S	C	S	G		333
TTG	CCT	CAT	TTG	CAG	TCA	GGG	TCT	GAT	GTT	GTA	TGG	CTT	GAT	GGT	GTC	TCC	TGC	TCC	GGT		1026
N	E	S	F	L	W	D	C	R	H	S	G	T	V	N	F	D	C	L	H		353
AAT	GAA	TCT	TTT	CTT	TGG	GAC	TGC	AGA	CAT	TCC	GGA	ACC	GTC	AAT	TTT	GAC	TGT	CTT	CAT		1086



Q	N	D	V	S	V	I	C	S	D	G	A	D	L	E	L	R	L	A	D	373
CAA	AAC	GAT	GTG	TCT	GTG	ATC	TGC	TCA	GAT	GGA	GCA	GAT	TTG	GAA	CTG	CGA	CTA	GCA	GAT	1146
G	S	N	N	C	S	G	R	V	E	V	R	I	H	E	Q	W	W	T	I	393
GGA	AGT	AAC	AAT	TGT	TCA	GGG	AGA	GTA	GAG	GTG	AGA	ATT	CAT	GAA	CAG	TGG	TGG	ACA	ATA	1206
C	D	Q	N	W	K	N	E	Q	A	L	V	V	C	K	Q	L	G	C	P	413
TGT	GAC	CAG	AAC	TGG	AAG	AAT	GAA	CAA	GCC	CTT	GTG	GTT	TGT	AAG	CAG	CTA	GGA	TGT	CCG	1266
F	S	V	F	G	S	R	R	A	K	P	S	N	E	A	R	D	I	W	I	433
TTC	AGC	GTC	TTT	GGC	AGT	CGT	CGT	GCT	AAA	CCT	AGT	AAT	GAA	GCT	AGA	GAC	ATT	TGG	ATA	1326
N	S	I	S	C	T	G	N	E	S	A	L	W	D	C	T	Y	D	G	K	453
AAC	AGC	ATA	TCT	TGC	ACT	GGG	AAT	GAG	TCA	GCT	CTC	TGG	GAC	TGC	ACA	TAT	GAT	GGA	AAA	1386
A	K	R	T	C	F	R	R	S	D	A	G	V	I	C	S	D	K	A	D	473
GCA	AAG	CGA	ACA	TGC	TTC	CGA	AGA	TCA	GAT	GCT	GGA	GTA	ATT	TGT	TCT	GAT	AAG	GCA	GAT	1446
L	D	L	R	L	V	G	A	H	S	P	C	Y	G	R	L	E	V	K	Y	493
CTG	GAC	CTA	AGG	CTT	GTC	GGG	GCT	CAT	AGC	CCC	TGT	TAT	GGG	AGA	TTG	GAG	GTG	AAA	TAC	1506
Q	G	E	W	G	T	V	C	H	D	R	W	S	T	R	N	A	A	V	V	513
CAA	GGA	GAG	TGG	GGG	ACT	GTG	TGT	CAT	GAC	AGA	TGG	AGC	ACA	AGG	AAT	GCA	GCT	GTT	GTG	1566
C	K	Q	L	G	C	G	K	P	M	H	V	F	G	M	T	Y	F	K	E	533
TGT	AAA	CAA	TTG	GGA	TGT	GGA	AAG	CCT	ATG	CAT	GTG	TTT	GGT	ATG	ACC	TAT	TTT	AAA	GAA	1626
A	S	G	P	I	W	L	D	D	V	S	C	I	G	N	E	S	N	I	W	553
GCA	TCA	GGA	CCT	ATT	TGG	CTG	GAT	GAC	GTT	TCT	TGC	ATT	GGA	AAT	GAG	TCA	AAT	ATC	TGG	1686
D	C	E	H	S	G	W	G	K	H	N	C	V	H	R	E	D	V	I	V	573
GAC	TGT	GAA	CAC	AGT	GGA	TGG	GGA	AAG	CAT	AAT	TGT	GTA	CAC	AGA	GAG	GAT	GTG	ATT	GTA	1746
T	C	S	G	D	A	T	W	G	L	R	L	V	G	G	S	N	R	C	S	593
AAC	TGC	TCA	GGT	GAT	GCA	ACA	TGG	GGC	CTG	AGG	CTG	GTG	GGC	GGC	AGC	AAC	CGC	TGC	TCG	1806
G	R	L	E	V	Y	F	Q	G	R	W	G	T	V	C	D	D	G	W	N	613
GGA	AGA	CTG	GAG	GTG	TAC	TTT	CAA	GGA	CGG	TGG	GGC	ACA	GTG	TGT	GAT	GAC	GGC	TGG	AAC	1866
S	K	A	A	A	V	V	C	S	Q	L	D	C	P	S	S	I	I	G	M	633
AGT	AAA	GCT	GCA	GCT	GTG	GTG	TGT	AGC	CAG	CTG	GAC	TGC	CCA	TCT	TCT	ATC	ATT	GGC	ATG	1926
G	L	G	N	A	S	T	G	Y	G	K	I	W	L	D	D	V	S	C	D	653
GGT	CTG	GGA	AAC	GCT	TCT	ACA	GGA	TAT	GGA	AAA	ATT	TGG	CTC	GAT	GAT	GTT	TCC	TGT	GAT	1986
G	D	E	S	D	L	W	S	C	R	N	S	G	W	G	N	N	D	C	S	673
GGA	GAT	GAG	TCA	GAT	CTC	TGG	TCA	TGC	AGG	AAC	AGT	GGG	TGG	GGA	AAT	AAT	GAC	TGC	AGT	2046
H	S	E	D	V	G	V	I	C	S	D	A	S	D	M	E	L	R	L	V	693
CAC	AGT	GAA	GAT	GTT	GGA	GTG	ATC	TGT	TCT	GAT	GCA	TCG	GAT	ATG	GAG	CTG	AGG	CTT	GTG	2106
G	G	S	S	R	C	A	G	K	V	E	V	N	V	Q	G	A	V	G	I	713
GGT	GGA	AGC	AGC	AGG	TGT	GCT	GGA	AAA	GTT	GAG	GTG	AAT	GTC	CAG	GGT	GCC	GTG	GGA	ATT	2166
L	C	A	N	G	W	G	M	N	I	A	E	V	V	C	R	Q	L	E	C	733
CTG	TGT	GCT	AAT	GGC	TGG	GGA	ATG	AAC	ATT	GCT	GAA	GTT	GTT	TGC	AGG	CAA	CTT	GAA	TGT	2226

Fig. 2C

10/53

G	S	A	I	R	V	S	R	E	P	H	F	T	E	R	T	L	H	I	L	753
GGG	TCT	GCA	ATC	AGG	GTC	TCC	AGA	GAG	CCT	CAT	TTC	ACA	GAA	AGA	ACA	TTA	CAC	ATC	TTA	2286
M	S	N	S	G	C	T	G	G	E	A	S	L	W	D	C	I	R	W	E	773
ATG	TCG	AAT	TCT	GGC	TGC	ACT	GGA	GGG	GAA	GCC	TCT	CTC	TGG	GAT	TGT	ATA	CGA	TGG	GAG	2346
W	K	Q	T	A	C	H	L	N	M	E	A	S	L	I	C	S	A	H	R	793
TGG	AAA	CAG	ACT	GCG	TGT	CAT	TTA	AAT	ATG	GAA	GCA	AGT	TTG	ATC	TGC	TCA	GCC	CAC	AGG	2406
Q	P	R	L	V	G	A	D	M	P	C	S	G	R	V	E	V	K	H	A	813
CAG	CCC	AGG	CTG	GTT	GGA	GCT	GAT	ATG	CCC	TGC	TCT	GGA	CGT	GTT	GAA	GTG	AAA	CAT	GCA	2466
D	T	W	R	S	V	C	D	S	D	F	S	L	H	A	A	N	V	L	C	833
GAC	ACA	TGG	CGC	TCT	GTC	TGT	GAT	TCT	GAT	TTC	TCT	CTT	CAT	GCT	GCC	AAT	GTG	CTG	TGC	2526
R	E	L	N	C	G	D	A	I	S	L	S	V	G	D	H	F	G	K	G	853
AGA	GAA	TTA	AAT	TGT	GGA	GAT	GCC	ATA	TCT	CTT	TCT	GTG	GGA	GAT	CAC	TTT	GGA	AAA	GGG	2586
N	G	L	T	W	A	E	K	F	Q	C	E	G	S	E	T	H	L	A	L	873
AAT	GGT	CTA	ACT	TGG	GCC	GAA	AAG	TTC	CAG	TGT	GAA	GGG	AGT	GAA	ACT	CAC	CTT	GCA	TTA	2646
C	P	I	V	Q	H	P	E	D	T	C	I	H	S	R	E	V	G	V	V	893
TGC	CCC	ATT	GTT	CAA	CAT	CCG	GAA	GAC	ACT	TGT	ATC	CAC	AGC	AGA	GAA	GTT	GGA	GTT	GTC	2706
C	S	R	Y	T	D	V	R	L	V	N	G	K	S	Q	C	D	G	Q	V	913
TGT	TCC	CGA	TAT	ACA	GAT	GTC	CGA	CTT	GTG	AAT	GGC	AAA	TCC	CAG	TGT	GAC	GGG	CAA	GTG	2766
E	I	N	V	L	G	H	W	G	S	L	C	D	T	H	W	D	P	E	D	933
GAG	ATC	AAC	GTG	CTT	GGA	CAC	TGG	GGC	TCA	CTG	TGT	GAC	ACC	CAC	TGG	GAC	CCA	GAA	GAT	2826
A	R	V	L	C	R	Q	L	S	C	G	T	A	L	S	T	T	G	G	K	953
GCC	CGT	GTT	CTA	TGC	AGA	CAG	CTC	AGC	TGT	GGG	ACT	GCT	CTC	TCA	ACC	ACA	GGA	GGA	AAA	2886
Y	I	G	E	R	S	V	R	V	W	G	H	R	F	H	C	L	G	N	E	973
TAT	ATT	GGA	GAA	AGA	AGT	GTT	CGT	GTG	TGG	GGA	CAC	AGG	TTT	CAT	TGC	TTA	GGG	AAT	GAG	2946
S	L	L	D	N	C	Q	M	T	V	L	G	A	P	P	C	I	H	G	N	993
TCA	CTT	CTG	GAT	AAC	TGT	CAA	ATG	ACA	GTT	CTT	GGA	GCA	CCT	CCC	TGT	ATC	CAT	GGA	AAT	3006
T	V	S	V	I	C	T	G	S	L	T	Q	P	L	F	P	C	L	A	N	1013
ACT	GTC	TCT	GTG	ATC	TGC	ACA	GGA	AGC	CTG	ACC	CAG	CCA	CTG	TTT	CCA	TGC	CTC	GCA	AAT	3066
V	S	D	P	Y	L	S	A	V	P	E	G	S	A	L	I	C	L	E	D	1033
GTA	TCT	GAC	CCA	TAT	TTG	TCT	GCA	GTT	CCA	GAG	GGC	AGT	GCT	TTG	ATC	TGC	TTA	GAG	GAC	3126
K	R	L	R	L	V	D	G	D	S	R	C	A	G	R	V	E	I	Y	H	1053
AAA	CGG	CTC	CGC	CTA	GTG	GAT	GGG	GAC	AGC	CGC	TGT	GCC	GGG	AGA	GTA	GAG	ATC	TAT	CAC	3186
D	G	F	W	G	T	I	C	D	D	G	W	D	L	S	D	A	H	V	V	1073
GAC	GGC	TTC	TGG	GGC	ACC	ATC	TGT	GAT	GAC	GGC	TGG	GAC	CTG	AGC	GAT	GCC	CAC	GTG	GTG	3246
C	Q	K	L	G	C	G	V	A	F	N	A	T	V	S	A	H	F	G	E	1093
TGT	CAA	AAG	CTG	GGC	TGT	GGA	GTG	GCC	TTC	AAT	GCC	ACG	GTC	TCT	GCT	CAC	TTT	GGG	GAG	3306
G	S	G	P	I	W	L	D	D	L	N	C	T	G	T	E	S	H	L	W	1113
GGG	TCA	GGG	CCC	ATC	TGG	CTG	GAT	GAC	CTG	AAC	TGC	ACA	GGA	ACG	GAG	TCC	CAC	TTG	TGG	3366

11/53

Q	C	P	S	R	G	W	G	Q	H	D	C	R	H	K	E	D	A	G	V	1133
CAG	TGC	CCT	TCC	CGC	GGC	TGG	GGG	CAG	CAC	GAC	TGC	AGG	CAC	AAG	GAG	GAC	GCA	GGG	GTC	3426
I	C	S	E	F	T	A	L	R	L	Y	S	E	T	E	T	E	S	C	A	1153
ATC	TGC	TCA	GAA	TTC	ACA	GCC	TTG	AGG	CTC	TAC	AGT	GAA	ACT	GAA	ACA	GAG	AGC	TGT	GCT	3486
G	R	L	E	V	F	Y	N	G	T	W	G	S	V	G	R	R	N	I	T	1173
GGG	AGA	TTG	GAA	GTC	TTC	TAT	AAC	GGG	ACC	TGG	GGC	AGC	GTC	GGC	AGG	AGG	AAC	ATC	ACC	3546
T	A	I	A	G	I	V	C	R	Q	L	G	C	G	E	N	G	V	V	S	1193
ACA	GCC	ATA	GCA	GGC	ATT	GTG	TGC	AGG	CAG	CTG	GGC	TGT	GGG	GAG	AAT	GGA	GTT	GTC	AGC	3606
L	A	P	L	S	K	T	G	S	G	F	M	W	V	D	D	I	Q	C	P	1213
CTC	GCC	CCT	TTA	TCT	AAG	ACA	GGC	TCT	GGT	TTC	ATG	TGG	GTG	GAT	GAC	ATT	CAG	TGT	CCT	3666
K	T	H	I	S	I	W	Q	C	L	S	A	P	W	E	R	R	I	S	S	1233
AAA	ACG	CAT	ATC	TCC	ATA	TGG	CAG	TGC	CTG	TCT	GCC	CCA	TGG	GAG	CGA	AGA	ATC	TCC	AGC	3726
P	A	E	E	T	W	I	T	C	E	D	R	I	R	V	R	G	G	D	T	1253
CCA	GCA	GAA	GAG	ACC	TGG	ATC	ACA	TGT	GAA	GAT	AGA	ATA	AGA	GTG	CGT	GGA	GGA	GAC	ACC	3786
E	C	S	G	R	V	E	I	W	H	A	G	S	W	G	T	V	C	D	D	1273
GAG	TGC	TCT	GGG	AGA	GTG	GAG	ATC	TGG	CAC	GCA	GGC	TCC	TGG	GGC	ACA	GTG	TGT	GAT	GAC	3846
S	W	D	L	A	E	A	E	V	V	C	Q	Q	L	G	C	G	S	A	L	1293
TCC	TGG	GAC	CTG	GCC	GAG	GCG	GAA	GTG	GTG	TGT	CAG	CAG	CTG	GGC	TGT	GGC	TCT	GCT	CTG	3906
A	A	L	R	D	A	S	F	G	Q	G	T	G	T	I	W	L	D	D	M	1313
GCT	GCC	CTG	AGG	GAC	GCT	TCG	TTT	GGC	CAG	GGA	ACT	GGA	ACC	ATC	TGG	TTG	GAT	GAC	ATG	3966
R	C	K	G	N	E	S	F	L	W	D	C	H	A	K	P	W	G	Q	S	1333
CGG	TGC	AAA	GGA	AAT	GAG	TCA	TTT	CTA	TGG	GAC	TGT	CAC	GCC	AAA	CCC	TGG	GGA	CAG	AGT	4026
D	C	G	H	K	E	D	A	G	V	R	C	S	G	Q	S	L	K	S	L	1353
GAC	TGT	GGA	CAC	AAG	GAA	GAT	GCT	GGC	GTG	AGG	TGC	TCT	GGA	CAG	TCG	CTG	AAA	TCA	CTG	4086
N	A	S	S	G	H	L	A	L	I	L	S	S	I	F	G	L	L	L	L	1373
AAAT	GCC	TCC	TCA	GGT	CAT	TTA	GCA	CTT	ATT	TTA	TCC	AGT	ATC	TTT	GGG	CTC	CTT	CTC	CTG	4146
V	L	F	I	L	F	L	T	W	C	R	V	Q	K	Q	K	H	L	P	L	1393
GTT	CTG	TTT	ATT	CTA	TTT	CTC	ACG	TGG	TGC	CGA	GTT	CAG	AAA	CAA	AAA	CAT	CTG	CCC	CTC	4206
R	V	S	T	R	R	R	G	S	L	E	E	N	L	F	H	E	M	E	T	1413
AGA	GTT	TCA	ACC	AGA	AGG	AGG	GGT	TCT	CTC	GAG	GAG	AAT	TTA	TTC	CAT	GAG	ATG	GAG	ACC	4266
C	L	K	R	E	D	P	H	G	T	R	T	S	D	D	T	P	N	H	G	1433
TGC	CTC	AAG	AGA	GAG	GAC	CCA	CAT	GGG	ACA	AGA	ACC	TCA	GAT	GAC	ACC	CCC	AAC	CAT	GGT	

TGATAATAAAATTGAATTATGTATATCACTGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAACGGACGCGTGGGTCG 4626

AC 4628

Fig. 2E

[illegible]

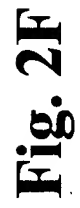


Fig. 2G

	10	20	30	40	50	60	70
Hum	MMLPQNSWHIDFGRCCCHQNLFSAVVTCILLNNSCFLISSFNGTDLELRLVNGDGPCSGTVEVKFQGQWG						
	:	:	:	:	:	:	:
WCI	MAL-----GR---HLSLRGL---CVLLLTGT--MVG---GQALELRLKDGVHRCGRVEVKHQGEWG						
		10	20	30	40	50	
	80	90	100	110	120	130	
Hum	TVCGDGNWTTASTVVCQQLGCPFSFAMFRFGQAVTR-HGKIWLDDVSCYGNESALWECQH---REWGSHN						
	:	:	:	:	:	:	:
WCI	TVDGYRWTLKDASVVCQQLGCGAAIG-FPGGAYFGPGLPIWLLYTSCEGTSTVSDCHEHSNIKDYRNDG						
	60	70	80	90	100	110	
	140	150	160	170	180	190	200
Hum	CYHGEDVGVNVCYGEANLGLRLVDGNNSCSGRVEVKFQERWGTICDDGWNLTAAVVCQQLGCPSSFISSG						
	:	:	:	:	:	:	:
WCI	YNHGRDAGVVCSSG----FVRLAGGDGPCSGRVEVHSGEAWIPVSDGNFTLATAQIIICAEELGCGKAVSVLG						
	120	130	140	150	160	170	180
	210	220	230	240	250	260	270
Hum	VWNSPAVLRPIWLDDILCQGNELALWNCRHRGWGNHDCSHNEDVTLTCYDSSDLELRLVGGTNRCMGRVE						
	:	:	:	:	:	:	:
WCI	HELFRRESSAQVWAEFRCEGEEPELWVCPRVPCPGGTCHHSGSAQVVCSSAYSEVRL-MTNGSSQCEGQVE						
	190	200	210	220	230	240	250
	280	290	300	310	320	330	340
Hum	LKIQGRWGTVCCHHKWNNAADVCKQLGCGTALHFAGLPHLQSGSDVVWLDGVSCSGNESFLWDCRHS GT						
	:	:	:	:	:	:	:
WCI	MNISGQWRALCASHWSLANANVICRQLGCGVAISTPGGPHLVEEGDQILTARFHCSGAESFLWSCPVTAL						
	260	270	280	290	300	310	320
	350	360	370	380	390	400	410
Hum	VNFDCLEHNDVSVICSDGADLELRLADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVCQQLGCPFSV						
	:	:	:	:	:	:	:
WCI	GGPDCSHGNTASVICS-GNQI-----QVLPQCND-----SV						
	330	340				350	
	420	430	440	450	460	470	480
Hum	FGSRRAKPSNEARDIWINISICTGNESALWDCTYDGKAKRTCFRRSDAGVICSDKADLDLRLVGAHSPCY						
	:	:	:	:	:	:	:
WCI	-----SQPTGSA-----ASEDSA---PY-----CSDSRQL--RLVDGGGPCA						
	360				370	380	
	490	500	510	520	530	540	550
Hum	GRLEVKYQGEWGTVCCHDRWSTRNAADVCKQLGCGKPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCE						
	:	:	:	:	:	:	:
WCI	GRVEILDQGSWGTICDDGWLDLDARVVCQQLGCGEALNATGSAHFGAGSGPIWLDNLNCTGKESHVWRCP						
	390	400	410	420	430	440	450

	560	570	580	590	600	610	620
Hum	HSGWGKHNCVHREDVIVTCSGDATWGLRLVGGSNRCSGRLEVFYQGRWGTVCDDGWSKAAAVVCSQLDC						
WCI	SRGWGQHNCRHKQDAGVICS--EFLALRMVSEDQQCAGWLEVFYNGTWGSVCRNPMEDITVSTICRQLGC						
	460	470	480	490	500	510	520
Hum	630	640	650	660	670	680	690
WCI	PSSIIGMGLGNASTGYGKIWLDDVSCDGEDSLWSCRNSGWGNNDCSHSEDVGVICSDASDMELRLVGGG						
	530	540	550	560	570	580	590
Hum	700	710	720	730	740	750	760
WCI	SRCAGKVEVNVQGAUGILCANGWGMNIAEVVCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASL						
	600	610	620	630	640	650	660
Hum	770	780	790	800	810	820	830
WCI	WDCIRWEWKQTACHLNMEASLICSABRQPRLVGADMPGSGRVEVKHADTWRSVCDSDFSLHAANVLCREL						
	670	680	690	700	710	720	730
Hum	840	850	860	870	880	890	900
WCI	NCGDAISLSVGDHFGKGNGLTWAEEKFQCEGSETHALALCPVQHPEDTCIHSREVGVVCSRYTDVRLV-NG						
	740	750	760	770	780	790	800
Hum	910	920	930	940	950	960	970
WCI	KSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGKYGIGERSVRVWGHFRFCHLGNESL						
	810	820	830	840	850	860	870
Hum	980	990	1000	1010	1020	1030	1040
WCI	LDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAVPEGSALICLEDKRLRLVDGDSRC						
	880	890	900	910	920	930	940
Hum	1050	1060	1070	1080	1090	1100	1110
WCI	AGRVEIYHDGFWGTICDDGWDLSDAHVVCQKLGCGVAFNATVSAHFGEESGPIWLDDLNCTGTESHLWQC						
	950	960	970	980	990	1000	1010
Hum	1120	1130	1140	1150	1160	1170	1180
WCI	PSRGWGQHDCRHKEDAGVICSEFTALRLYSETETESACAGRLEVFYNGTWGSGVRNITTALAGIVCRQLG						
	1020	1030	1040	1050	1060	1070	

Fig. 2H

	1190	1200	1210	1220	1230	1240
Hum	CGENGVVSLAPLSKTGSGFMWVDDIQCPKTHISIWQCLSA PWERRISSPAEETWITCEDR-----					
WCI	CGDSGSLNTSVGLREGSRPRWVDLIQCRKMDTSLWQCPSPGPWKYSSCSPKEEAYISCEGRRPKSCPTAAA					
	1080	1090	1100	1110	1120	1130 1140

	1250	1260	1270	1280	1290	1300
Hum	-----IRVRGGDTECSGRVEIWHAGSWGTVCDSDSLAEAEVVCQQLGCGSALAALRDASFGQGTGTIW					
WCI	CTDREKLRLRGGDSECSGRVEVWHNGSWGTVCDSDSLAEAEVVCQQLGCGQALEAVRSAAFGPGNGSIW					
	1150	1160	1170	1180	1190	1200 1210

	1310	1320	1330	1340	1350	1360
Hum	LDDMRCKGNESFLWDCHAKPWGQSDCGHKEDAGVRCG-----QSLKSLNASSGHLALI					
WCI	LDEVQCGGRESSLWDCVAEPWGQSDCKHEEDAGVRCSGVRTTLPTTTAGTRTTSNSLPGIFSLPGVLCCLI					
	1220	1230	1240	1250	1260	1270 1280

	1370	1380	1390	1400	1410
Hum	LSSIEGLLLLVLFILFLTWCRVQK-----QKHLPLRVS-----TRRRG-----SLEENLFHEME				
WCI	LGSLLFLVLVILVTQLRW-RAERRALSSYEDALAEAVYEELDYLLTQKEGLGSPDQMTDVPDENYDDAE				
	1290	1300	1310	1320	1330 1340 1350

	1420	1430	1440
Hum	TC-----LKREDPHGTRTSD-----DTPNHGCEAS-----DTSLLGV		
WCI	EVPVPGTPSPSQGNEEEVPPEKEDGVRSSQTGSFLNFSREANPGEGEESFWLLQGKKG DAGYDDVELSA		
	1360	1370	1380 1390 1400 1410 1420

	1450
Hum	LPASEAT-K
WCI	LGTSPVTFS
	1430

Fig. 2I



Fig. 2J

	10	20	30	40	50	60	70
Hum	ATGATGCTGCCTCAAACTCGTGGCATATTGATTTTGAAGATGCTGCTGTCTCATCAGAACCTTTTCTCTG						
	...	....	...		.....	...	...
WCI	ATG-----GCTC-TGG-----GCAGACA-----CCTCT-CCCTG						
			10			20	

	80	90	100	110	120	130	140
Hum	CTGTGGTAACTTGCATCCTGCTCCTGAATTCCTGCTTTCTCATCAGCAGTTTAAATGGAACAGATTTGGA						
	...	...	...	...	...	...	...
WCI	C-GGGGACTCT-GTGTCTCTCCTCCT-----CGGCA---C-----CATGGTGGTGGTCAAGCTCTGGA						
	30	40	50		60	70	80

	150	160	170	180	190	200	210
Hum	GTTGAGGCTGGTCAATGGAGACGGTCCCTGCTCTGGGACAGTGGAGGTGAAATTCAGGGACAGTGGGGG						
	...	...	...	...	...	...	...
WCI	GCTGAGGTTGAAGGATGGAGTCCATCGCTGTGAGGGGAGAGTGAAGTGAAGCACCAAGGAGAATGGGGC						
	90	100	110	120	130	140	150

	220	230	240	250	260	270
Hum	ACTGTGTGTGATGATGGGTGGAACACTACTGCCT-CAACTGTCGTGTGCAAACAGCTTGGATGTCCATTT					
	...	...	...	...	...	...
WCI	ACAGTGGATGGTTACAGGTGGA-CATTGAAGGATGCATCTGTAGTGTGCAGACAGCTGGGGTGTGGAGCT					
	160	170	180	190	200	210

	280	290	300	310	320	330	340
Hum	TCTTTCGCCATGTTTCGTTTTTGGACAAGCCGTGA--CTAGACATGGAAAAATTTGGCTTGATGATGTTTC						
	...	...	...	...	...	...	...
WCI	GCCATTG--GTTTTCTGGAGGGGCTTATTTTGGGCCAGGACTTGGCCCCATTGGCTTTTGTATACTTC						
	220	230	240	250	260	270	280

	350	360	370	380	390	400	410
Hum	CTGTTATGGAAATGAGTCAGCTCTCTGGAATGTCAACACCGGAATGGGAAGCCATAACTGTTATCAT						
	...	...	...	...	...	...	...
WCI	ATGTGAAGGGACAGAGTCAACTGTCTGAGTGTGAGCAT-TCTAATATTAAAGAC-TATC-GTAATGAT						
	290	300	310	320	330	340	350

	420	430	440	450	460	470	480
Hum	GGAGAAGATGTTGGTGTGAACGTGTTATGGTGAAGCCAA-TCTGGGTTTGAG--GCTAG-TGGATGGAAAC						
	...	...	...	...	...	...	...
WCI	GGCTATAATCATGGTCGGGA---TGCTGGAGTAGTCTGCTCAGGATTTGTGCGTCTGGCTGGAGGGGATG						
	360	370	380	390	400	410	420

	490	500	510	520	530	540	550
Hum	AACTCCTGTTTCAGGGAGAGTGGAGGTGAAATTCAGAAAGGTGGGGGACTATATGTGATGATGGGTGGA						
	...	...	...	...	...	...	...
WCI	GAC-CCTGCTCAGGGCGAGTAGAAGTGCATT--CTGGAGAAGCTTGGATCCCAGTGT-CTGATGGGAACT						
	430	440	450	460	470	480	

	560	570	580	590	600	610	620
Hum	ACTTGAATACTGCTGCCGTGGTGTGCAGGCAACTAGGATGTCCATCTTCTTTATTTCTTCTGGAGTTGT						
WCI	TCACACTTGCCACTGCC-----CAG-----ATCATCTGT-----GCAGAGTTGGG						
	490	500			510	520	
	630	640	650	660	670	680	690
Hum	TAATAGCCCTGCTGTATTGCGCCCCATTTGGCTGGATGACATTTTATGCCAGGGGAATGAGTTGGCACT-						
WCI	TTGTGGC-----AAGGCTG--TGTCTGT--CCTGGGACATGAG---CTCTT						
	530		540		550	560	
	700	710	720	730	740	750	760
Hum	CTGGAATTGCAGACATCGTGGATGGGGAAATCATGACTGCAGTCACAATGAGGATGTCACATTAAC TTGT						
WCI	CAGAGAGTCCAGT-GCC-----CAGGTCTG--GGC---TGAAGAGTTCA-----GG						
	570	580		590		600	
	770	780	790	800	810	820	830
Hum	TATGATAGTAGTCACTTTGAACTAAGGCTTGTAGGTGGAAC TAACCGCTGTATGGGGAGAGTAGAGCTGA						
WCI	TGTGAGGGGGAGGAGCCTGAGCT---CT-----GGGTCTGCCC-CAGAGTG-----CCCTG-						
	610	620	630		640		650
	840	850	860	870	880	890	900
Hum	AAATCCAAGGAAGGTGGGGGACCGTATGCCACCATAAGTGGAAACAATGCTGCAGCTGATGTCGTATGCAA						
WCI	---TCCA-----GGGGGCACGTGT--CACCACA-GTGGATC--TGCT-CAGGTTGTTTGTTCAGCAT						
		660	670	680	690	700	
	910	920	930	940	950	960	970
Hum	GCAGTTGGGATGTGGAACCGCACTTCACTTCGCTGGCTTGCCCTCATTTGCAGTCAGGGTCTGATGTTGTA						
WCI	ACT-----CAGAAGTCCGGCTCATGACAA-AC-GGCT--CCTC-TCAG-TGTGAAGGGCAGGTGGAGAT						
	710	720	730		740	750	760
	980	990	1000	1010	1020	1030	1040
Hum	TGGCTTGATGGTGTCTCCTGCTCCGGTAATGAATCTTTCTTTGGGACTGCAGACATTCCGGAACCGTCA						
WCI	GAACATT-----TCTG-GACAATGGAGAGCGCTCTGTGCCTCCC-ACTGGAGTCTGGCCAATGCC---A						
	770		780	790	800	810	820
	1050	1060	1070	1080	1090	1100	1110
Hum	ATTTTGA CTGTCTTCATCAAAACGATGTGTCTGTGATCTGCTCAGATGGAGCAGATTTGGA ACTGCGACT						
WCI	ATGTTATCTGTCTGCTCAGCTCGGCTGTGGAGTTGCCATCTCCACCCCGGAG-----GACCAC-ACT						
	830	840	850	860	870		880
	1120	1130	1140	1150	1160	1170	1180
Hum	AGCAGATGGAAGTAACAATTGTTTCAGGGAGAGTAGAGGTGAGAATTCA-TGAACAGTGGTGGACAATATG						
WCI	TG---GTGGAAGAAG---GTGATCAG--ATCCTAACAGCCCGATTTCAGTCTCTG---GGGC---TG						
	890		900	910	920	930	

Fig. 2K

	1190	1200	1210	1220	1230	1240	1250
Hum	TGACCAGAACTGGAAGAATGAACAAGCCCTTGTGGTTTGTAAAGCAGCTAGGATGTCCGTTTCAGCGTCTTT						
WCI	AGTCCT-TCCTGTGGAGTTGT-----CCT-GTGACT-----GCC-CTGGGTGGTCCTGACTGTTCCCAT						
	940	950	960		970	980	990

	1260	1270	1280	1290	1300	1310	1320
Hum	GGCAG-TCGTCGTGCTAAACCTAGTAATGAAGCTAGAGACATTTGGATAAACAGCATATCTTGCACTGGG						
WCI	GGCAACACAGCCCTCTGTGATCTGCTCAGGAAACCAGATCCAGGTGCTTCCCCAGTGCAACGA-CTCCG--						
	1000	1010	1020	1030	1040	1050	1060

	1330	1340	1350	1360	1370	1380	1390
Hum	AATGAGTCAGCTCTCTGGGACTGCACATATGATGGAAAAGCAAAGCGAACATGCTTCCGAAGATCAGATG						
WCI	--TGTCTCAACCTACAGGCTCTGC-----GGC-----CTCAGAGGACA-GCGCCC-----CCTACTG						
	1070	1080		1090	1100		

	1400	1410	1420	1430	1440	1450	1460
Hum	CTGGAGTAATTTGTTCTGATAAGGCAGATCTGGACCTAAGGCCTGTCGGGGCTCATAGCCCCCTGTTATGG						
WCI	CTCAGA-----CAG--CAGGCAGCTCCG--CCTGGTG--GACGGGG-GC--GGTCCCTGCGCCGG						
	1110	1120	1130		1140	1150	1160

	1470	1480	1490	1500	1510	1520	
Hum	GAGATTGGAGGTGAAATACCAAGGAGAGTGGGGGACTGTGTGTATGACAGATGGAGCACAAGG-AATGC						
WCI	GAGAGTGGAGATCCTTGACCAGGGCTCCTGGGGCACCATCTGTGATGACGGCTGGGAC-CTGGACGATGC						
	1170	1180	1190	1200	1210	1220	

	1530	1540	1550	1560	1570	1580	1590
Hum	A-GCTGTTGTGTGTAAACAATTGGGATGTGGA-AAGCCTATGCATGTGTTTGGTATGACCTATTTTAAAG						
WCI	CCGC-GTGGTGTGCAGGCAGCTGGGCTGTGGAGAAGCCCTCA-ATGCCACGGGGTCTGCTCACTTCGGGG						
	1230	1240	1250	1260	1270	1280	1290

	1600	1610	1620	1630	1640	1650	1660
Hum	AAGCATCAGGACCTATTTGGCTGGATGACGTTTCTTGCAATTGGAAATGAGTCAAATATCTGGGACTGTGA						
WCI	CAGGATCAGGGCCCATCTGGTTGGACAACCTGAACTGCACAGGAAAGGAGTCCCACGTGTGGAGGTGCC						
	1300	1310	1320	1330	1340	1350	1360

	1670	1680	1690	1700	1710	1720	1730
Hum	ACACAGTGGATGGGGAAAGCATAATTGTGTACACAGAGAGGATGTGATTGTAACCTGCTCAGGTGATGCA						
WCI	TTCCCGGGGCTGGGGGAGCACAACCTGCAGACACAAGCAGGACGCGGGGTCATCTGCTCAG--AGTTC-						
	1370	1380	1390	1400	1410	1420	1430

	1740	1750	1760	1770	1780	1790	1800
Hum	ACATGGGGCCTGAGGCTGGTGGGCGGCAGCAACCGCTGCTCGGGAAGACTGGAGGTGTACTTTCAAGGAC						
WCI	-CT--GGCCCTCAGGATGGTGAAGTGAAGACAGCAGTGTGCTGGGTGGCTGGAAGTTTTCTACAATGGGA						
	1440	1450	1460	1470	1480	1490	1500

Fig. 2L

```

1810      1820      1830      1840      1850      1860      1870
Hum  GGTGGGGCACAGTGTGTGATGACGGCTGGAACAGTAAAGCTGCAGCTGTGGTGTGTAGCCAGCTGGACTG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WCI  CCTGGGGCAGTGTCTGCCGTAACCCCATGGAAGACATCACTGTGTCCACGATCTGCAGACAGCTTGGCTG
      1510      1520      1530      1540      1550      1560      1570

1880      1890      1900      1910      1920      1930      1940
Hum  CCCATCTTCTATCATTTGGCATGGGTCTG-GGAAACGCTTCTA-CAGGATATGGAAAATTTGGCTCGATG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WCI  T--GGGGACAGTGAACCCCTCAACTCTTCTGTTGCTCTTAGAGAAGGTTTTAGGCCACAGTGGGTGGAT-
      1580      1590      1600      1610      1620      1630

1950      1960      1970      1980      1990      2000      2010
Hum  ATGTTTCCTGTGATGGAGATGAGTCAGATCTCTGGTCATGCAGGAACAGTGGGTG--GGGAAATAATGAC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WCI  -AGAATCCAGTGTGCGAAACTGACACCTCTCT---CTGGCAGTGTCTTCTGACCCTTGGAATTACAAC
      1640      1650      1660      1670      1680      1690      1700

2020      2030      2040      2050      2060      2070      2080
Hum  TGCAGTCACAGTGAAGATGTTGGAGTG-ATCTGTTCTGATG-CATCGGATATGGAGCTGAGGCTTGTGGG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WCI  T-CATGCTCTCCAAGGAGGAAGCCTATATCTGGTGTGCAGACAGCAGACA--GATCCGC--CTGGTGGG
      1710      1720      1730      1740      1750      1760

2090      2100      2110      2120      2130      2140      2150
Hum  TGGAAGCAGCAGGTGTGCTGGAAAGTTGAGGTGAATGTCCAGGGTGCCGTGGGAATTCTGTGTGCTAAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WCI  TGGAGGTGGTGTGCTGCTCTGGGAGAGTGGAGATCCTTGACCAGGGCTCCTGGGGCACCATCTGTGTATGAC
      1770      1780      1790      1800      1810      1820      1830

2160      2170      2180      2190      2200      2210      2220
Hum  GGCTGGGGAATGAACATTGCTGAAGTTGTTTGCAGGCAACTTGAATGTGGGTCTGCAATCAGGGTCTCCA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WCI  CGCTGGGACCTGGACGATGCCCGTGTGGTGTGCAAGCAGCTGGGCTGTGGAGAAGC---CCTGGACGCCA
      1840      1850      1860      1870      1880      1890      1900

2230      2240      2250      2260      2270      2280
Hum  GAGA-GCCTCATTTACAGAA--AGAACATTACACATCTTAATGTGCAATTCTGGCTGCACTGGAGGGGA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WCI  CTGTCTCTTCTTCTTCGGGACGGGATCAGGGCCCATCTGGCTGGATGAAGTGAAGTGCAGAGGAGAGGA
      1910      1920      1930      1940      1950      1960      1970

2290      2300      2310      2320      2330      2340      2350
Hum  AGCCTCTCTCTGGGATTGTATACGATGGGAGTGGAAACAG-ACTGCGTGTCAATTTAAATATGGAAGCAAG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WCI  GTCCCAAGTATGGAGGTGCCCTTCTGGGGATGGCGGCAACACAAC-TGCAATCATCAAGAAGATGCAGG
      1980      1990      2000      2010      2020      2030      2040

2360      2370      2380      2390      2400      2410      2420
Hum  TTTGATCTGCTCAGCCACAGGCAGCCAGGCTGGTGGAGCTGATATGCCCTGCTCTGGACGTGTTGAA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WCI  AGTCATCTGCTCAGGATTTGTGC-----GTCTGGCTGGAGGAGATGGACCCTGCTCAGGGCGAGTAGAA
      2050      2060      2070      2080      2090      2100

```

Fig. 2M

	2430	2440	2450	2460	2470	2480	2490
Hum	GTGAAACATGCAGACACATGGCGCTCTGTCTGTGATTCTGATTTCTCTCTTCATGCTGCCAATGT--GCT						
WCI	GTGCATTCTGGAGAAGCCTGGACCCAGTGTCTGATGGAACTTCACACTCCCCACTGCCCAGGTCACTCT						
	2110	2120	2130	2140	2150	2160	2170
	2500	2510	2520	2530	2540	2550	2560
Hum	GTGCAGAGAATTAAATTGTGGAGATGCCATATCTCTTTCTGTGGGAGATCACTTTGGAAAAGGG-AATGG						
WCI	GTGCAGAGC--TGGGATGTGGCAAGGCTGTGTCT-GTCCTGGGACACATGCCATTGAGAGAGTCCGATGG						
	2180	2190	2200	2210	2220	2230	2240
	2570	2580	2590	2600	2610	2620	2630
Hum	TCTAACTTGGGCGCGAAAAGTTCCAGTGTGAAGGGAGTGAACTCACCTTGCAATTATGCCCCATTGTTCAA						
WCI	CCAGGTCTGGGCTGAAGAGTTCCAGGTGTGATGGGGGGGAGCCTGAGCTCTGGTCTGCCCCAGAGTGCCC						
	2250	2260	2270	2280	2290	2300	2310
	2640	2650	2660	2670	2680	2690	2700
Hum	CATCCGGAAGACACTTGTATCCACAGCAGAGAAGTTGGAGTTGTCTGTTCCCGATATACAGATGTCCGAC						
WCI	TGTCCAGGAGGCACATGTCTCCACAGTGGAGCTGCTCAGGTTGTCTGTTTCAGTGTACACAGAAGTCCAGC						
	2320	2330	2340	2350	2360	2370	2380
	2710	2720	2730	2740	2750	2760	2770
Hum	TTGTGAATGGCAAATCC---CAGTGTGACGGGCAAGTGGAGATCAACGTGCT-TGGACACTGGGGCTCAC						
WCI	TTATGAAAAACGGCACCTCTCAATGTGAGGGGCGAGGTGGAGAT-GAAGATCTCTGGACGATGGAGAGCGC						
	2390	2400	2410	2420	2430	2440	2450
	2780	2790	2800	2810	2820	2830	2840
Hum	TGTGTGACACCCACTGGGACCCAGAAGATGCCCGTGTCTATGCAGACAGCTCAGCTGTGGGACTGCTCT						
WCI	TCTGTGCCTCCCACTGGAGTCTGGCCAATGCCAATGTTGTCTGTCTGTCGTCAGCTCGGCTGTGGAGTCGCCAT						
	2460	2470	2480	2490	2500	2510	2520
	2850	2860	2870	2880	2890	2900	2910
Hum	CTCAACCACAGGAGGAAAATATATTGGAGAAAGAAGTGTTCGTGTGTGGGGACACAGGTTTCATTGCTTA						
WCI	CTCCACCCCCAGAGGACCACACTTGGTGGAAAGGAGGTGATCAGATCTCAACAGCCCAATTTCACTGCTCA						
	2530	2540	2550	2560	2570	2580	2590
	2920	2930	2940	2950	2960	2970	2980
Hum	GGGAATGAGTCACTTCTGGATAACTGTCAAATGACAGTTCTTGGAGCACCTCCCTGTATCCATGGAAATA						
WCI	GGGGCTGAGTCCTTCCTGTGGAGTTGTCTGTGACTGCCTTGGGTGGGCTGACTGTTCCCATGGCAACA						
	2600	2610	2620	2630	2640	2650	2660
	2990	3000	3010	3020	3030	3040	3050
Hum	CTGTCTCTGTGATCTGCACAGGAAGCCTGACCCAGCCACTGTTTCCATGCCTCGCAAATGTATCTGACCC						
WCI	CAGCCTCTGTGATCTGCTCAGGAAACCACACCCAGGTGCTGCCCCAGTGCAACGACTTCCTGTCTCAACC						
	2670	2680	2690	2700	2710	2720	2730

Fig. 2N

	3060	3070	3080	3090	3100	3110	3120
Hum	ATATTTGTCTGCAGTTCAGAGGGCAGTGCTTTGATCTGCTTAGAGGACAAACGGCTCCGCCTAGTGGAT						
WCI	TGCAGGCTCTGCGGCCTCAGAGGAGAGTTCTCCCTACTGCTCAGACAGCAGGCAGCTCCGCCTGGTGGAG						
	2740	2750	2760	2770	2780	2790	2800
	3130	3140	3150	3160	3170	3180	3190
Hum	GGGGACAGCCGCTGTGCCGGGAGAGTAGAGATCTATCACGACGGCTTCTGGGGCACCATCTGTGATGACG						
WCI	GGGGGCGGTCCCTGCGGCGGGAGAGTGGAGATCCTTGACCAGGGCTCCTGGGGCACCATCTGTGATGATG						
	2810	2820	2830	2840	2850	2860	2870
	3200	3210	3220	3230	3240	3250	3260
Hum	GCTGGGACCTGAGCGATGCCACGTGGTGTGTCAAAGCTGGGCTGTGGAGTGGCCTTCAATGCCACGGT						
WCI	ACTGGGACCTGGACGATGCCCGTGTGGTGTGCAGGCAGCTGGGCTGTGGAGAAGCCCTCAATGCCACGGG						
	2880	2890	2900	2910	2920	2930	2940
	3270	3280	3290	3300	3310	3320	3330
Hum	CTCTGCTCATTGTTGGGGAGGGGTCAGGGCCCATCTGGCTGGATGACCTGAAGTGCACAGGAACGGAGTCC						
WCI	GTCTGCTCATTGTTGGGGCAGGATCAGGGCCCATCTGGCTGGACGACCTGAAGTGCACAGGAAGGAGTCC						
	2950	2960	2970	2980	2990	3000	3010
	3340	3350	3360	3370	3380	3390	3400
Hum	CACTTGTGGCAGTGCCCTTCCCCGGGCTGGGGGCAGCAGACTGCAGGCACAAGGAGGACGCAGGGGTCA						
WCI	CACGTGTGGAGGTGCCCTTCCCCGGGGCTGGGGGCAGCAGACTGCAGACACAAGGAGGACGCCGGGGTCA						
	3020	3030	3040	3050	3060	3070	3080
	3410	3420	3430	3440	3450	3460	3470
Hum	TCTGCTCAGAATTCACAGCCTTGAGGCTCTACAGTGAAGTGAAGCAGAGAGCTGTGCTGGGAGATTGGA						
WCI	TCTGCTCAGAGTTCCTGGCCCTCAGGAT---GGTGAG-CGAGGACCAGCAG-TGTGCTGGGTGGCTGGA						
	3090	3100	3110	3120	3130	3140	
	3480	3490	3500	3510	3520	3530	3540
Hum	AGTCTTCTATAACGGGACCTGGGGCAGCGTCGGCAGGAGGAACATCACCACAGCCATAGCAGGCATTGTG						
WCI	GGTTTTCTACAACGGGACCTGGGGCAGTGTCTGCCGAGCCCCATGGAAGATATCACTGTGTCCGTGATC						
	3150	3160	3170	3180	3190	3200	3210
	3550	3560	3570	3580	3590	3600	
Hum	TGCAGGCAGCTGGGCTGTGGGGAGAAATGGAGTTGTGAGCCTCGCCCCTTTA--TCT-AAGACAGGCTCTG						
WCI	TGCAGACAGCTTGGATGTGGGGACAGTGA--AGTCT-CAACACCTCTGTTGGTCTCAGGGAAGGTTCTA						
	3220	3230	3240	3250	3260	3270	3280
	3610	3620	3630	3640	3650	3660	3670
Hum	GTTTCATGTGGGTGGATGACATTTCAGTGTCTCTAAACGCATATCTCCATATGGCAGTGCCTGTCTGCCCC						
WCI	GACCCCGGTGGGTAGATTTAATTCAGTGTCTCGGAAATGGATACCTCTCTCTGGCAGTGTCTCTCTGGCCC						
	3290	3300	3310	3320	3330	3340	3350

Fig. 20

Fig. 2P

Fig. 2P

Fig. 2Q



GTCGACCCACGCGTCCGGTCTGTGGCTGAGC																				M	A	L	P	A	L	G	L	D	P	W	S		12
ATG GCC CTC CCA GCC CTG GGC CTG GAC CCC TGG AGC																																67	
L	L	G	L	F	L	F	Q	L	L	Q	L	L	L	P	T	T	T	A	G	32													
CTC	CTG	GGC	CTT	TTC	CTC	TTC	CAA	CTG	CTT	CAG	CTG	CTG	CTG	CCG	ACG	ACG	ACC	GCG	GGG	127													
G	G	G	Q	G	P	M	P	R	V	R	Y	Y	A	G	D	E	R	R	A	52													
GGA	GGC	GGG	CAG	GGG	CCC	ATG	CCC	AGG	GTC	AGA	TAC	TAT	GCA	GGG	GAT	GAA	CGT	AGG	GCA	187													
L	S	F	F	H	Q	K	G	L	Q	D	F	D	T	L	L	L	S	G	D	72													
CTT	AGC	TTC	TTC	CAC	CAG	AAG	GGC	CTC	CAG	GAT	TTT	GAC	ACT	CTG	CTC	CTG	AGT	GGT	GAT	247													
G	N	T	L	Y	V	G	A	R	E	A	I	L	A	L	D	I	Q	D	P	92													
GGA	AAT	ACT	CTC	TAC	GTG	GGG	GCT	CGA	GAA	GCC	ATT	CTG	GCC	TTG	GAT	ATC	CAG	GAT	CCA	307													
G	V	P	R	L	K	N	M	I	P	W	P	A	S	D	R	K	K	S	E	112													
GGG	GTC	CCC	AGG	CTA	AAG	AAC	ATG	ATA	CCG	TGG	CCA	GCC	AGT	GAC	AGA	AAA	AAG	AGT	GAA	367													
C	A	F	K	K	K	S	N	E	T	Q	C	F	N	F	I	R	V	L	V	132													
TGT	GCC	TTT	AAG	AAG	AAG	AGC	AAT	GAG	ACA	CAG	TGT	TTC	AAC	TTC	ATC	CGT	GTC	CTG	GTT	427													
S	Y	N	V	T	H	L	Y	T	C	G	T	F	A	F	S	P	A	C	T	152													
TCT	TAC	AAT	GTC	ACC	CAT	CTC	TAC	ACC	TGC	GGC	ACC	TTC	GCC	TTC	AGC	CCT	GCT	TGT	ACC	487													
R	I	E	L	Q	D	S	Y	L	L	P	I	S	E	D	K	V	M	E	G	172													
TTE	ATT	GAA	CTT	CAA	GAT	TCC	TAC	CTG	TTG	CCC	ATC	TCG	GAG	GAC	AAG	GTC	ATG	GAG	GGA	547													
K	G	Q	S	P	F	D	P	A	H	K	H	T	A	V	L	V	D	G	M	192													
AAA	GGC	CAA	AGC	CCC	TTT	GAC	CCC	GCT	CAC	AAG	CAT	ACG	GCT	GTC	TTG	GTG	GAT	GGG	ATG	607													
H	Y	S	G	T	M	N	N	F	L	G	S	E	P	I	L	M	R	T	L	212													
CTC	TAT	TCT	GGT	ACT	ATG	AAC	AAC	TTC	CTG	GGC	AGT	GAG	CCC	ATC	CTG	ATG	CGC	ACA	CTG	667													
G	S	Q	P	V	L	K	T	D	N	F	L	R	W	L	H	H	D	A	S	232													
GGA	TCC	CAG	CCT	GTC	CTC	AAG	ACC	GAC	AAC	TTC	CTC	CGC	TGG	CTG	CAT	CAT	GAC	GCC	TCC	727													
F	V	A	A	I	P	S	T	Q	V	V	Y	F	F	F	E	E	T	A	S	252													
TTT	GTG	GCA	GCC	ATC	CCT	TCG	ACC	CAG	GTC	GTC	TAC	TTC	TTC	TTC	GAG	GAG	ACA	GCC	AGC	787													
E	F	D	F	F	E	R	L	H	T	S	R	V	A	R	V	C	K	N	D	272													
GAG	TTT	GAC	TTC	TTT	GAG	AGG	CTC	CAC	ACA	TCG	CGG	GTG	GCT	AGA	GTC	TGC	AAG	AAT	GAC	847													
V	G	G	E	K	L	L	Q	K	K	W	T	T	F	L	K	A	Q	L	L	292													
GTG	GGC	GGC	GAA	AAG	CTG	CTG	CAG	AAG	AAG	TGG	ACC	ACC	TTC	CTG	AAG	GCC	CAG	CTG	CTC	907													
C	T	Q	P	G	Q	L	P	F	N	V	I	R	H	A	V	L	L	P	A	312													
TGC	ACC	CAG	CCG	GGG	CAG	CTG	CCC	TTC	AAC	GTC	ATC	CGC	CAC	GCG	GTC	CTG	CTC	CCC	GCC	967													
D	S	P	T	A	P	H	I	Y	A	V	F	T	S	Q	W	Q	V	G	G	33													

K	Y	K	E	L	N	K	E	T	S	R	W	T	T	Y	R	G	P	E	T	372
AAA	TAC	AAA	GAG	TTG	AAC	AAA	GAA	ACT	TCA	CGC	TGG	ACT	ACT	TAT	AGG	GGC	CCT	GAG	ACC	1147
N	P	R	P	G	S	C	S	V	G	P	S	S	D	K	A	L	T	F	M	392
AAC	CCC	CGG	CCA	GGC	AGT	TGC	TCA	GTG	GGC	CCC	TCC	TCT	GAT	AAG	GCC	CTG	ACC	TTC	ATG	1207
K	D	H	F	L	M	D	E	Q	V	V	G	T	P	L	L	V	K	S	G	412
AAG	GAC	CAT	TTC	CTG	ATG	GAT	GAG	CAA	GTG	GTG	GGG	ACG	CCC	CTG	CTG	GTG	AAA	TCT	GGC	1267
V	E	Y	T	R	L	A	V	E	T	A	Q	G	L	D	G	H	S	H	L	432
GTG	GAG	TAT	ACA	CGG	CTT	GCA	GTG	GAG	ACA	GCC	CAG	GGC	CTT	GAT	GGG	CAC	AGC	CAT	CTT	1327
V	M	Y	L	G	T	T	T	G	S	L	H	K	A	V	V	S	G	D	S	452
GTC	ATG	TAC	CTG	GGA	ACC	ACC	ACA	GGG	TCG	CTC	CAC	AAG	GCT	GTG	GTA	AGT	GGG	GAC	AGC	1387
S	A	H	L	V	E	E	I	Q	L	F	P	D	P	E	P	V	R	N	L	472
AGT	GCT	CAT	CTG	GTG	GAA	GAG	ATT	CAG	CTG	TTC	CCT	GAC	CCT	GAA	CCT	GTT	CGC	AAC	CTG	1447
Q	L	A	P	T	Q	G	A	V	F	V	G	F	S	G	G	V	W	R	V	492
CAG	CTG	GCC	CCC	ACC	CAG	GGT	GCA	GTG	TTT	GTA	GGC	TTC	TCA	GGA	GGT	GTC	TGG	AGG	GTG	1507
P	R	A	N	C	S	V	Y	E	S	C	V	D	C	V	L	A	R	D	P	512
CCC	CGA	GCC	AAC	TGT	AGT	GTC	TAT	GAG	AGC	TGT	GTG	GAC	TGT	GTC	CTT	GCC	CGG	GAC	CCC	1567
H	C	A	W	D	P	E	S	R	T	C	C	L	L	S	A	P	N	L	N	532
CAC	TGT	GCC	TGG	GAC	CCT	GAG	TCC	CGA	ACC	TGT	TGC	CTC	CTG	TCT	GCC	CCC	AAC	CTG	AAC	1627
S	W	K	Q	D	M	E	R	G	N	P	E	W	A	C	A	S	G	P	M	552
TCC	TGG	AAG	CAG	GAC	ATG	GAG	CGG	GGG	AAC	CCA	GAG	TGG	GCA	TGT	GCC	AGT	GGC	CCC	ATG	1687
S	R	S	L	R	P	Q	S	R	P	Q	I	I	K	E	V	L	A	V	P	572
AGC	AGG	AGC	CTT	CGG	CCT	CAG	AGC	CGC	CCG	CAA	ATC	ATT	AAA	GAA	GTC	CTG	GCT	GTC	CCC	1747
N	S	I	L	E	L	P	C	P	H	L	S	A	L	A	S	Y	Y	W	S	592
AAC	TCC	ATC	CTG	GAG	CTC	CCC	TGC	CCC	CAC	CTG	TCA	GCC	TTG	GCC	TCT	TAT	TAT	TGG	AGT	1807
H	G	P	A	A	V	P	E	A	S	S	T	V	Y	N	G	S	L	L	L	612
CAT	GGC	CCA	GCA	GCA	GTC	CCA	GAA	GCC	TCT	TCC	ACT	GTC	TAC	AAT	GGC	TCC	CTC	TTG	CTG	1867
I	V	Q	D	G	V	G	G	L	Y	Q	C	W	A	T	E	N	G	F	S	632
ATA	GTG	CAG	GAT	GGA	GTT	GGG	GGT	CTC	TAC	CAG	TGC	TGG	GCA	ACT	GAG	AAT	GGC	TTT	TCA	1927
Y	P	V	I	S	Y	W	V	D	S	Q	D	Q	T	L	A	L	D	P	E	652
TAC	CCT	GTG	ATC	TCC	TAC	TGG	GTG	GAC	AGC	CAG	GAC	CAG	ACC	CTG	GCC	CTG	GAT	CCT	GAA	1987
L	A	G	I	P	R	E	H	V	K	V	P	L	T	R	V	S	G	G	A	672
CTG	GCA	GGC	ATC	CCC	CGG	GAG	CAT	GTG	AAG	GTC	CCG	TTG	ACC	AGG	GTC	AGT	GGT	GGG	GCC	2047
A	L	A	A	Q	Q	S	Y	W	P	H	F	V	T	V	T	V	L	F	A	692
GCC	CTG	GCT	GCC	CAG	CAG	TCC	TAC	TGG	CCC	CAC	TTT	GTC	ACT	GTC	ACT	GTC	CTC	TTT	GCC	2107
L	V	L	S	G	A	L	I	I	L	V	A	S	P	L	R	A	L	R	A	712
TTA	GTG	CTT	TCA	GGA	GCC	CTC	ATC	ATC	CTC	GTG	GCC	TCC	CCA	TTG	AGA	GCA	CTC	CGG	GCT	2167
R	G	K	V	Q	G	C	E	T	L	R	P	G	E	K	A	P	L	S	R	732
CGG	GGC	AAG	GTT	CAG	GGC	TGT	GAG	ACC	CTG	CGC	CCT	GGG	GAG	AAG	GCC	CCG	TTA	AGC	AGA	2227

27/53

[illegible]

Fig. 3D

	10	20	30	40	50	60	70
Hum.	MALPALGLDPWSLLGLFLFQLLQLLPTTTAGGGGQGPMRVRYYAGDERRALSFFHQKGLQDFDTLLLS						
Mur.	MALPSLGQDSWSLLRVFFQLFLPLSLPPASGTGGQGPMRVRKYHAGDGHRLSFFQQKGLRDFDTLLLS						
	10	20	30	40	50	60	70
	80	90	100	110	120	130	140
Hum.	GDGNTLYVGAREAILALDIQDPGVPRLLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLY						
Mur.	DDGNTLYVGARETVLALNIQNPGIPRLKNMIPWPASERKKTECAFKKKSNETQCFNFIRVLVSYNATHLY						
	80	90	100	110	120	130	140
	150	160	170	180	190	200	210
Hum.	TCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYSGTMNIFLGSEPIILMR						
Mur.	ACGTFAFSPACTFIELQDSLLLPILIDKVMGKGQSPLTFTSTQAVLVDGMLYSGTMNIFLGSEPIILMR						
	150	160	170	180	190	200	210
	220	230	240	250	260	270	280
Hum.	TLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFEETASEFDFFERLHTRSARVAVCKNDVGGEKLLQ						
Mur.	TLGSHPVLTDFLRLHADASFVAAIPSTQVVYFFFEETASEFDFFEELYISRAQVCKNDVGGEKLLQ						
	220	230	240	250	260	270	280
	290	300	310	320	330	340	350
Hum.	KKWTTFLKAQLLCTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVF						
Mur.	KKWTTFLKAQLLCAQPGQLPFNIIRHAVLLPADSPSVSRIYAVFTSQWQVGGTRSSAVCAFSLLDIERVF						
	290	300	310	320	330	340	350
	360	370	380	390	400	410	420
Hum.	KGKYKELNKETSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAV						
Mur.	KGKYKELNKETSRWTTYRGSEVSPRPGSCSMGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAV						
	360	370	380	390	400	410	420
	430	440	450	460	470	480	490
Hum.	ETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLPDPEPVRNLQLAPTQGAVFVGFSGGVW						
Mur.	ESARGLDGSSHVMYLGSTGSLHKAVVPQDSSAYLVEEIQSPDSEPVRNLQLAPAQGAVFAGFSGGIW						
	430	440	450	460	470	480	490
	500	510	520	530	540	550	560
Hum.	RVPRANC SVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRPOS						
Mur.	RVPRANC SVYESCVDCVLARDPHCAWDPESTRCSLLSGST-KPWKQDMERGNPEWVCTRGPMSRPRQS						
	500	510	520	530	540	550	
	570	580	590	600	610	620	630
Hum.	RPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASSTVYNGSLLLVQDGVGGLYQCWATENG						
Mur.	PPQLIKEVLTVPNSILELRCPHLSALASYHWSHGRAKISEASATVYNGSLLLVQDGVGGLYQCWATENG						
	560	570	580	590	600	610	620
	640	650	660	670	680	690	700
Hum.	FSYPVISYWVDSQDQTLALDPELAGIPREHVKVLTRVSGGAALAAQSYWPHFVTVTVLFAVLVSGALI						
Mur.	YSYPVVSYWVDSQDQPLALDPELAGVPRERQVPLTRVGGGASMAAQRSYWPHFLIVTVLLAIVLLGLVT						
	630	640	650	660	670	680	690
	710	720	730	740	750	760	
Hum.	ILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA						
Mur.	LLLASPLGALRARGKVQCGMLPPEKAPLSRDQHLQPSKDHRTSASDVDADNNHLGAEVA						
	700	710	720	730	740	750	760

Fig. 3E

Hum. GTCG-AC-CC-----ACG-----CGTCCGGT-----CTGTGGCTGAGCATGGC  
 Mur. CTCGGACGCCTGGGTTAGGGGTCTGTACTGCTGGGGAACCATCTGGTGACCATCTCAGGCTGACCATGGC  
 10 20 30 40 50 60 70

Hum. CCTCCCAGCCCTGGGCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACGCTTC-AGCTGCT  
 Mur. CCTACCATCCCTGGGCCAGGACTCATGGAGTCTCCTGCGTGTCTTTTCTTCCAACCT-CTTCCTGCTGCC  
 80 90 100 110 120 130

Hum. GCTGCCGACGACGACCGGGGGGAGGCGGGCAGGGGCCATGCCAGGGTCAGATACTATGCAGGGGAT  
 Mur. ATCACTGCCACCTGCTTCTGGGACTGGTGGTCAGGGGCCATGCCAGAGTCAAATACCATGCTGGAGAC  
 140 150 160 170 180 190 200

Hum. GAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTG  
 Mur. GGGCACAGGGCCCTCAGCTTCTTCCAACAAAAGGCCCTCCGAGACTTTGACACGCTGCTCCTGAGTGACG  
 210 220 230 240 250 260 270

Hum. ATGGAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCC  
 Mur. ATGGCAACACTCTCTATGTGGGGGCTCGAGAGACCGTCTTGGCCTTGAATATCCAGAACCAGGAATCCC  
 280 290 300 310 320 330 340

Hum. CAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAG  
 Mur. AAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGAGAGAAAAAGACCGAATGTGCCTTTAAGAAGAAG  
 350 360 370 380 390 400 410

Hum. AGCAATGAGACACAGTGTTCAACTTCATCCGTGTCTGGTTCCTTACAATGTACCCATCTCTACACCT  
 Mur. AGCAATGAGACACAGTGTTCAACTTCATTCGAGTCTGGTCTCTTACAATGCTACTCACCCTCTATGCCT  
 420 430 440 450 460 470 480

Hum. GCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGATTCCTACCTGTGCCCATCTC  
 Mur. GTGGGACCTTTGCCTTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGATTCCTCCTGTGCCCATCTT  
 490 500 510 520 530 540 550

Hum. GGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCTTTGACCCCGCTCACAAGCATACG-GCTGTCTT  
 Mur. GATAGACAAGGTCATGGACGGGAAGGGCCAAAGCCC-TTTGACCCTGTTCAACAAGCACACAAGCTGTCTT  
 560 570 580 590 600 610 620

Hum. GGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACA  
 Mur. GGTGCGATGGGATGCTTTATTCCGGCACCATGAACAACTTCCTGGGCAGGAGCCCATCCTGATGCGGACA  
 630 640 650 660 670 680 690

Hum. CTGGGATCCCAGCCTGTCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGG  
 Mur. CTGGGATCCCATCCTGTTCTCAAGACTGACATCTTCTTACGCTGGCTGCACGCGGATGCCTCCTTCGTGG  
 700 710 720 730 740 750 760

Hum. 740 750 760 770 780 790 800  
CAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGA  
Mur. 770 780 790 800 810 820 830  
CAGCCATTCCATCCACCCAGGTCGTCTATTCTTCTTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGA

Hum. 810 820 830 840 850 860 870  
GAGGCTCCACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAG  
Mur. 840 850 860 870 880 890 900  
AGAGCTGTATATATCCAGGGTGGCTCAAGTCTGCAAGAACGACGTGGGCGGTGAAAAGCTGCTGCAGAAG

Hum. 880 890 900 910 920 930 940  
AAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCC  
Mur. 910 920 930 940 950 960 970  
AAGTGGACCACCTTCCTCAAAGCCCAGTTGCTCTGCGCTCAGCCAGGGCAGCTGCCATTCAACATCATCC

Hum. 950 960 970 980 990 1000 1010  
GCCACGCGGTCTGCTCCCCGCCGATTCTCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTG  
Mur. 980 990 1000 1010 1020 1030 1040  
GCCACGCGGTCTGCTGCGCCGCCGATTCTCCCTCTGTTTCCCGCATCTACGCAGTCTTTACCTCCCAGTG

Hum. 1020 1030 1040 1050 1060 1070 1080  
GCAGGTTGGCGGGACCCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTTGGACATTGAACGTGCTTTAAG  
Mur. 1050 1060 1070 1080 1090 1100 1110  
GCAGGTTGGCGGGACCCAGGAGCTCAGCAGTCTGTGCCTTCTCTCTCACGACATTGAGCGAGTCTTTAAA

Hum. 1090 1100 1110 1120 1130 1140 1150  
GGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCC  
Mur. 1120 1130 1140 1150 1160 1170 1180  
GGGAAGTACAAGGAGCTGAACAAGGAGACCTCCCGCTGGACCACTTACCAGGGCTCAGAGGTGAGCCCGA

Hum. 1160 1170 1180 1190 1200 1210 1220  
GGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCTGTAT  
Mur. 1190 1200 1210 1220 1230 1240 1250  
GGCCAGGCAGTTGCTCCATGGGCCCCCTCCTCTGACAAAGCCTTGACCTTCATGAAGGACCATTTCTGTAT

Hum. 1230 1240 1250 1260 1270 1280 1290  
GGATGAGCAAGTGGTGGGGACGCCCCCTGCTGGTGAATCTGGCGTGGAGTATACACGGCTTCAGTGGAG  
Mur. 1260 1270 1280 1290 1300 1310 1320  
GGATGAGCAGTGGTAGGAACACCCCTGCTGGTGAAGTCTGGTGTGGAGTACACACGGCTTCAGTGGAG

Hum. 1300 1310 1320 1330 1340 1350 1360  
ACAGCCCAGGGCCTTGATGGGCACAGCCATCTGTCTATGTACCTGGGAACCACCACAGGGTGCCTCCACA  
Mur. 1330 1340 1350 1360 1370 1380 1390  
TCAGCTCGGGCCTTGATGGGAGCAGCCATGTGGTCTATGTATCTGGGTACCTCCACGGGTCCCTGCACA

Hum. 1370 1380 1390 1400 1410 1420 1430  
AGGCTGTGGTAAGTGGGGACAGCAGTGTCTATCTGGTGAAGAGATTACAGTGTTCCTGACCTGAACC  
Mur. 1400 1410 1420 1430 1440 1450 1460  
AGGCTGTGGTGCCTCAGGACAGCAGTGTCTATCTCGTGGAGGAGATTACAGTGTGAGCCCTGACTCTGAGCC

Hum. 1440 1450 1460 1470 1480 1490 1500  
TGTTTCGAAACCTGCAGCTGGCCCCCAGGGTGCAGTGTGTTAGGCTTCTCAGGAGGTGCTGGAGG  
Mur. 1470 1480 1490 1500 1510 1520 1530  
TGTTTCGAAACCTGCAGCTGGCCCCCAGGGTGCAGTGTGTTAGGCTTCTCAGGAGGTGCTGGAGG

Hum. 1510 1520 1530 1540 1550 1560 1570  
GTCCCCGAGCCAACCTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGGCCGGGACCCCCACTGTG  
Mur. 1540 1550 1560 1570 1580 1590 1600  
GTCCCCAGGGCAATTGCAGTGTCTACGAGAGCTGTGTGGACTGTGTGCTTGGCCAGGGACCCCTCACTGTG

	1580	1590	1600	1610	1620	1630	1640
Hum.	CCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACAT						
Mur.	CCTGGGACCCTGAATCAAGACTCTGCAGCCTTCTGTCTGGCTC-TACCAAGCCT--TGGAAGCAGGACAT						
	1610	1620	1630	1640	1650	1660	1670
	1650	1660	1670	1680	1690	1700	1710
Hum.	GGAGCGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGC						
Mur.	GGAACGCGGCAACCCGAGTGGGTATGCACCCGTGGCCCCATGGCCAGGAGCCCCGGCGTCAGAGCCCC						
	1680	1690	1700	1710	1720	1730	1740
	1720	1730	1740	1750	1760	1770	1780
Hum.	CCGCAATCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCTAG						
Mur.	CCTCAACTAATTAAAGAAGTCCTGACAGTCCCCAACTCCATCCTGGAGCTGCGCTGCCCCCACCTGTCTAG						
	1750	1760	1770	1780	1790	1800	1810
	1790	1800	1810	1820	1830	1840	1850
Hum.	CCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGG						
Mur.	CACTGGCCTCTTACCAGTGGAGTCATGGCCGAGCAAAATCTCAGAAGCCTCTGCTACCGTCTACAATGG						
	1820	1830	1840	1850	1860	1870	1880
	1860	1870	1880	1890	1900	1910	1920
Hum.	CTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGTCTCTACCAGTGTCTGGGCAACTGAGAATGGCTTT						
Mur.	CTCCCTCTTGCTGCTGCCGAGGATGGTGTGCGGGGCTCTACCAGTGTGTGGCGACTGAGAACGGCTAC						
	1890	1900	1910	1920	1930	1940	1950
	1930	1940	1950	1960	1970	1980	1990
Hum.	TCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAG						
Mur.	TCATACCCTGTGGTCTCCTATTGGGTAGACAGCCAGGACCAGCCCTGGCGCTGGACCCTGAGCTGGCGG						
	1960	1970	1980	1990	2000	2010	2020
	2000	2010	2020	2030	2040	2050	2060
Hum.	GCATCCCCCGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCA						
Mur.	GCGTTCCCCGTGAGCGTGTGCAGGTCCCGCTGACCAGGGTCGGAGGCGGAGCTTCCATGGCTGCCAGCG						
	2030	2040	2050	2060	2070	2080	2090
	2070	2080	2090	2100	2110	2120	2130
Hum.	GTCCTACTGGCCCCACTTTGTCACTGTCACTGTCTCTTTGCCTTAGTGCTTTTCAGGAGCCCTCATCATC						
Mur.	GTCCTACTGGCCCCATTTCTCATCGTTACCGTCTCTGGCCATCGTCTCCTGGGAGTGCTCACTCTC						
	2100	2110	2120	2130	2140	2150	2160
	2140	2150	2160	2170	2180	2190	2200
Hum.	CTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAGACCCTGCGCCCTG						
Mur.	CTCCTCGCTTCCCCACTGGGGGCGCTCGGGGCTCGGGGTAAGGTTTCAGGGCTGTGGGATGCTGCCCCCA						
	2170	2180	2190	2200	2210	2220	2230
	2210	2220	2230	2240	2250	2260	2270
Hum.	GGGAGAAAGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGA						
Mur.	GGGAAAAGGCTCCACTGAGCAGGGACCAGCACCTCCAGCCCTCCAAGGACCACAGGACCTCTGCCAGTGA						
	2240	2250	2260	2270	2280	2290	2300
	2280	2290	2300	2310	2320	2330	2340
Hum.	TGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGG-CCGGGGCTG--C						
Mur.	CGTAGATGCCGACAACAACCATCTGGGCGCCGAAGTGGCTTAAACA-GGGACACAGATCCGCAGCTGAGC						
	2310	2320	2330	2340	2350	2360	2370
	2350	2360	2370	2380	2390	2400	2410
Hum.	GGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAA						
Mur.	AGAGCAAGCCACTGGCCTTGTGGCTATGC---CAGGCACAG-----TGCCACTCT--						
	2380	2390	2400	2410			

2420 2430 2440 2450 2460 2470 2480  
 Hum. AGACCACCTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGTATGC  
 Mur. -GACCA-----GGGTAGGAG--GCT-CT-C-CTGCTA-ACGTGTGTAC-CTACAG-----C  
 2430 2440 2450 2460

2490 2500 2510 2520 2530 2540 2550  
 Hum. ACAGCAGTCTG-CCTCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCT  
 Mur. ACC-CAGTAGGTCCTCCCTGTGGGACTCTCTTCTGC-AAGCACATT-----GGGCT  
 2470 2480 2490 2500 2510

2560 2570 2580 2590 2600 2610  
 Hum. ACCCCAGACCTGCTCCTACACTGATA-TTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAG  
 Mur. GTCTCCATACCTGTACTTGTGCTGTGACAGGAAGAGCCAGAC-AGGTTTCTTTGATTGATTGACCCAA  
 2520 2530 2540 2550 2560 2570 2580

2620 2630 2640 2650 2660 2670 2680  
 Hum. GGACCCT-CCAGAAACACA-GTGTTCAGAGATCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTA  
 Mur. GAGCCCTGCCTGTAACAAACGTGCTCCAGGAGA-CCATGAAAGGTGTGGCTGTCT-GGGATTCTGTGGTG-  
 2590 2600 2610 2620 2630 2640 2650

2690 2700 2710 2720 2730 2740 2750  
 Hum. ATGAACACCAAACATCTAAACAATCATATGCTAA-CATGC---CAC--TCCTGGAACT-CCACTCTGAA  
 Mur. ACAAAC-CTAAGCATCCGAGCAAGCTGGGGCTATTCTGCAAACTCCATCCTGAACGCTGTCACTCTAGA  
 2660 2670 2680 2690 2700 2710 2720

2760 2770 2780 2790 2800 2810  
 Hum. ----GCTGCCGCTTTGGACACCAACACTCCCTTCT-CCCAGG-GTCATGCAGGGATCTGCTCCCTCCTGC  
 Mur. AGCAGCTGCTGCTTTGAACACCAGCCACCTCCTTCCCAAGAGTCTCTATGGAGTTGGC-CCCTTGTGT  
 2730 2740 2750 2760 2770 2780 2790

2820 2830 2840 2850 2860 2870 2880  
 Hum. TTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTCTCTGAAGTCTGACCACCTTTCTTCTTGC  
 Mur. TTCCTTTACCAGTCGGGCCATACCTGTTT---GGGAAGTCATCTCTGAAGTCTAACCACCTTCCTTCTTGG  
 2800 2810 2820 2830 2840 2850

2890 2900 2910 2920 2930 2940 2950  
 Hum. TTCAGTTGGGGCAGACTCTGATCCCT---TCTGCCCTGGCAGAAATGGCAGGGGTAATCTGAGCCTTCTTC  
 Mur. TTCAGTTGGACAGATTGTTATTATGCTCTGCCCCTGGCTAGAATGGGGGCATAATCTGAGCCTTGTTC  
 2860 2870 2880 2890 2900 2910 2920

2960 2970 2980 2990 3000 3010  
 Hum. ACTCCTTTACCC---TAGCTGACCCCTTCACCTCTCCC--CCTCCCTTTTCTTTGTTTGGGATTTCAGA  
 Mur. ---CCTTGTCCAGTGTGGCTGACCC-TTGACCTCTTCTTCTCC---TCCCTTTGTTTGGGATTTCAGA  
 2930 2940 2950 2960 2970 2980 2990

3020 3030 3040 3050 3060 3070 3080  
 Hum. AAAGTCTTGTGTCAGAGACTGTTTATTTTATTAAAAATATAAGGCTTAAAAAAAAAAAAAAAAAAAAA  
 Mur. AAAGTCTTGTGTCAGAGACAATTATTTTATTAAAAA-----AGATATAA  
 3000 3010 3020 3030

3090 3100  
 Hum. AAAAAAAGGGCGCCGC  
 Mur. GCTTTAAAG-----  
 3040



Fig. 3I

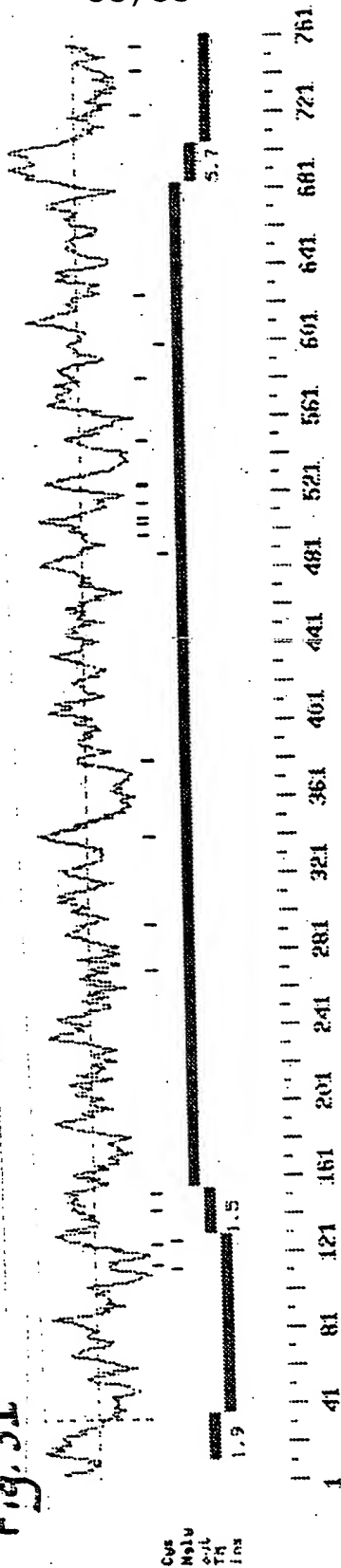


Fig. 4A

GTGACCCACGCGTCCGCGGACGCGTGGGGACGGCTCCCGGCTGCAGTCTGCCCCGCCCGCCCCGCGCGGGGGCCGAGTC 79

CGGAAGCGCGCCTGCGACCCGGCGTCCGGGCGCGCTGGAGAGGACGCGAGGAGCC	M	R	R	Q	P	A	6
ATG AGG CGC CAG CCT GCG	152						
K V A A L L L G L L L E C T E A K K H C	26						
AAG GTG GCG GCG CTG CTG CTC GGG CTG CTC TTG GAG TGC ACA GAA GCC AAA AAG CAT TGC	212						
W Y F E G L Y P T Y Y I C R S Y E D C C	46						
TGG TAT TTC GAA GGA CTC TAT CCA ACC TAT TAT ATA TGC CGC TCC TAC GAG GAC TGC TGT	272						
G S R C C V R A L S I Q R L W Y F W F L	66						
GGC TCC AGG TGC TGT GTG CGG GCC CTC TCC ATA CAG AGG CTG TGG TAC TTC TGG TTC CTT	332						
L M M G V L F C C G A G F F I R R R M Y	86						
CTG ATG ATG GGC GTG CTT TTC TGC TGC GGA GCC GGC TTC TTC ATC CGG AGG CGC ATG TAC	392						
P P P L I E E P A F N V S Y T R Q P P N	106						
CCC CCG CCG CTG ATC GAG GAG CCA GCC TTC AAT GTG TCC TAC ACC AGG CAG CCC CCA AAT	452						
P G P G A Q Q P G P P Y Y T D P G G P G	126						
CCC GGC CCA GGA GCC CAG CAG CCG GGG CCG CCC TAT TAC ACT GAC CCA GGA GGA CCG GGG	512						
M N P V G N S M A M A F Q V P P N S P Q	146						
ATG AAC CCT GTC GGG AAT TCC ATG GCA ATG GCT TTC CAG GTC CCA CCC AAC TCA CCC CAG	572						
G S V A C P P P P A Y C N T P P P P Y E	166						
GGG AGT GTG GCC TGC CCG CCC CCT CCA GCC TAC TGC AAC ACG CCT CCG CCC CCG TAC GAA	632						
Q V V K A K *	173						
CAG GTA GTG AAG GCC AAG TAG	653						
TTGGGTGCCCACGTGCAAGAGGAGAGACAGGAGAGGGCCTTTCCCTGGCCTTTCTGTCTTCGTTGATGTTCACTTCCAG	732						
GAACGGTCTCGTGGGCTGCTAAGGGCAGTTCTCTGATATCCTCACAGCAAGCACAGCTCTCTTTTCAGGCTTTCCATGG	811						
AGTACAATATATGAACTCACACTTTGTCTCCTCTGTGTGCTTCTGTTTCTGACGCAGTCTGTGCTCTCACATGGTAGTGT	890						
GGTGACAGTCCCCGAGGGCTGACGTCCTTACGGTGGCGTGACCAGATCTACAGGAGAGAGACTGAGAGGAAGAAGGCAG	969						
TGCTGGAGGTGCAGGTGGCATGTAGAGGGGCCAGGCCGAGCATCCCAGGCAAGCATCCTTCTGCCCCGGGTATTAATAGG	1048						
AAGCCCCATGCCGGGCGGCTCAGCCGATGAAGCAGCAGCCGACTGAGCTGAGCCCAGCAGGTCATCTGCTCCAGCCTGT	1127						
CCTCTCGTCAGCCTTCTCTTCCAGAAGCTGTGGAGAGACATTCAGGAGAGAGCAAGCCCCCTTGTTCATGTTTCTGTCT	1206						
CTGTTTCATATCCTAAAGATAGACTTCTCCTGCACCGCCAGGGAAGGGTAGCACGTGCAGCTCTCACC GCAGGATGGGGC	1285						
CTAGAATCAGGCTTGCCCTTGGAGGCCTGACAGTGATCTGACATCCACTAAGCAAATTTATTTAAATTCATGGGAAATCA	1364						
CTTCTGCCCCAAACTGAGACATTTGCATTTTGTGAGCTCTTGGTCTGATTTGGAGAAAGGACTGTTACCCATTTTTTTTG	1443						
GTGTGTTTATGGAAGTGCATGTAGAGCGTCTGCCCCCTTGAAATCAGACTGGGTGTGTGTCTTCCCTGGACATCACTGC	1522						
CTCTCCAGGGCATTCTCAGGCCCGGGGTCTCTTCCCTCAGGCAGCTCCAGTGGTGGGTCTGAAGGGTGTCTTCAAA	1601						
ACGGGGCACATCTGGCTGGGAAGTCACATGGACTCTTCCAGGGAGAGAGACCAGCTGAGGCGTCTCTCTCTGAGGTTGT	1680						

GTTGGGTCTAAGCGGGTGTGTGCTGGGCTCCAAGGAGGAGGAGCTTGCTGGGAAAAGACAGGAGAAGTACTGACTCAAC	1759
TGCACTGACCATGTTGTCTAATTAGAATAAAGAAGAAGTGGTCGGAAATGCACATTCCCTGGATAGGAATCACAGCTCA	1838
CCCCAGGATCTCACAGGTAGTCTCCTGAGTAGTTGACGGCTAGCGGGGAGCTAGTTCCGCCGCATAGTTATAGTGTGA	1917
TGTGTGAACGCTGACCTGTCTGTGTGCTAAGAGCTATGCAGCTTAGCTGAGGCGCCTAGATTACTAGATGTGCTGTAT	1996
CACGGGGAATGAGGTGGGGGTGCTTATTTTTTAATGAACTAATCAGAGCCTCTTGAGAAAATTGTTACTCATTGAACTGG	2075
AGCATCAAGACATCTCATGGAAGTGGATACGGAGTGATTTGGGTGTCCATGCTTTTCACTCTGAGGACATTTAATCGGAG	2154
AACCTCCTGGGGAATTTTGTGGGAGACACTTGGGAACAAAACAGACACCTGGGAAATGCAGTTGCAAGCACAGATGCTG	2233
CCACCAGTGTCTCTGACCACCCTGGTGTGACTGCTGACTGCCAGCGTGGTACCTCCCATGCTGCAGGCCCTCCATCTAAA	2312
TGAGACAACAAAGCACAAATGTTCACTGTTTACAACCAAGACAACCTGCGTGGGTCCAAACACTCCTCTTCCCTCCAGGTCA	2391
TTTGTTTTGCATTTTAAATGTCTTTATTTTTTGTAAATGAAAAAGCACACTAAGCTGCCCTGGAATCGGGTGCAGCTGA	2470
ATAGGCACCCAAAAGTCCGTGACTAAATTTTCGTTTGTCTTTTGTATAGCAAAATTATGTTAAGAGACAGTGATGGCTAGG	2549
GCTCAACAATTTTGTATTCCCATGTTTGTGTGAGACAGAGTTTGTTTTCCCTTGAACCTGGTTAGAATTGTGCTACTGT	2628
GAACGCTGATCCTGCATATGGAAGTCCCACCTTTGGTGACATTTCCCTGGCCATTCTTGTTTCCATTGTGTGGATGGTGGG	2707
TTGTGCCCACCTCCTGGAGTGAGACAGCTCCTGGTGTGTAGAATTCCCGGAGCGTCCGTGGTTCAGAGTAACTTGAAG	2786
CAGATCTGTGCATGCTTTTCCCTCTGCAACAATTGGGCTCGTTTCTCTTTTTTGTCTCTTTTGATAGGATCCTGTTTCCT	2865
ATGTGTGCAAAAATAAAAATAAATTTGGGCAA	2944
AAAAAAAAAAGGGCGGCCGC	2964

Fig. 4B

Fig. 4C

GTCGACCCACGCGTCCGGCCGCGCGTCTTCTGCCGGCTTCAGCTCGTATCCCCGGAGTCCACCCGCCCCGTCCCGGGGT 79  
 GCGGACTGGCCCTGAGCTGGCCGTACAGCCCGGCTTCGGACGGTCTCGCTGGAGCC ATG GGC CGC CGG CTC 151  
 M G R R L 5  
 G R V A A L L L G L L V E C T E A K K H 25  
 GGC AGG GTG GCG GCG CTG CTG CTC GGG CTG CTA GTG GAG TGC ACT GAG GCC AAA AAA CAT 211  
 C W Y F E G L Y P T Y Y I C R S Y E D C 45  
 TGC TGG TAT TTT GAA GGA CTC TAT CCC ACA TAC TAT ATA TGC CGT TCC TAT GAA GAC TGC 271  
 C G S R C C V R A L S I Q R L W Y F W F 65  
 TGT GGC TCC AGG TGC TGT GTG AGG GCC CTT TCC ATA CAG AGG CTG TGG TAT TTT TGG TTC 331  
 L L M M G V L F C C G A G F F I R R R M 85  
 CTG CTG ATG ATG GGT GTG CTG TTC TGC TGT GGT GCC GGT TTC TTC ATT CGC CGG CGC ATG 391  
 Y P P P L I E E P T F N V S Y T R Q P P 105  
 TAT CCG CCA CCA CTC ATT GAG GAG CCC ACA TTC AAT GTG TCC TAT ACC AGG CAG CCA CCA 451  
 N P A P G A Q Q M G P P Y Y T D P G G P 125  
 AAT CCT GCT CCA GGA GCA CAG CAA ATG GGA CCG CCA TAT TAC ACC GAC CCT GGA GGA CCC 511  
 G M N P V G N T M A M A F Q V Q P N S P 145  
 GGG ATG AAT CCT GTT GGC AAT ACC ATG GCT ATG GCT TTC CAG GTC CAG CCC AAT TCA CCT 571  
 H G G T T Y P P P P S Y C N T P P P P Y 165  
 CAC GGA GGC ACA ACT TAC CCA CCC CCT CCT TCC TAC TGC AAC ACG CCT CCA CCC CCC TAT 631  
 E Q V V K D K \* 173  
 GAA CAG GTG GTG AAG GAC AAG TAG 655  
 CAGATGCTACATCAAAGGCAAAGAGGATGGACAGGCCCTTTTGTGTTACCTTCCCATCCTCACCATACTTGCTGATAG 734  
 GGTGGTCCAAGGGAAAACCTTGGATATTCTCAAAGCAAGCCCAGCTCTCTTTCAAGTCTTTTGTGGAGGACATTTGAATC 813  
 CACACTGTCTCCTCTGTTGCTTCTGTTTCTGATGTAGTCTGTGCTCTCTGAGAGAGTGTGGCAACAGTCCCTGAGGGTT 892  
 GATATTCCTAGGGTGTCCAGGGTAGATCCTCGGGAGAGAGGCTAAGGGGAAAGGAAGGCATAGCCTGTGTGTTAGGGGG 971  
 CAGATAAAGTGGTCAGGCTGAGATAAGACTCACATGATGCAGTAGTTGGCAGTGAACCTCGAAGAGACACTATCCACCA 1050  
 TCCCAGCCCATTCTCCTAATAGAAGCTGTGGGGCTGTGTTGTTGATGCTCTTTGGTCTCCACTCACATTTTGAAAATAG 1129  
 GCTTTCCTCTGCAGGAATAGGAAAGACCCAAGTACATATTTGCTTCCACTTAAAAATGAGGGTCAGAACCAGGCCTCAG 1208  
 TTGGACATCTATAGTTAAATAAAGGCCATTAGAGAGGGGAAATCTTTAAGTTAGGGGAAATTCTCTAAATGGAGACATT 1287  
 GCGTTTTATGAATCATCGTCTGGCTTTTCTTTTGTGTCATGTATTGAAGTGAGGGTGTCTTTGAGATCAGATGGGGAG 1366  
 AGTGAACCTCTGCGGGGGGTGGGGTGTCTCTACTCAGAGGGCTCCAACACCCTTTTCTTAGGTAGTTCTGGTGATGGGTT 1445  
 TTATGGGCACTATAGAGCTGAGGGGCACATTAGGCCGGGTAGTTACATTGACCCTTGGAGAGGAAGAGGACAGCCAAAG 1524

AAAC TCAGCAAAGCAAGACCAGCATTGCTGAGTTAGAGCTAGGGTTGTATGTGATCCCAACAGAGATGTGCTGGCCTCA 1603  
 GAAGAGGGGACGTTTGTGGATAGAGCCGTGAAAACTACTTAGTTGCACAGATGACATAATCAAAAGTAGAGAAAGAAG 1682  
 TG TAGTTAGAGATGCCATTTCCAGGTGAGAATCAGAGCTCATCCATAGATTTACAAGTAGTGGCTGGAGTTAACAGTA 1761  
 TGGAGTTC TTTTCCCTTGCGTAGTTAGTCACGTTGATGTGTATTTAAACCCAGGTTGAGACCTTGTGTACTAAGAGCAA 1840  
 GGAAGTATAGCTAAGATGTCTAGATTATTTATATGTAGTATGCTGGGGAGTGGGGCTGCAAGGAAGGGGGCTGACATTG 1919  
 TAAATGAGAAAATCAGAGCCATTTGATAAACTGTTACTTGTGGATCAGGCATCCAAAAGTGTCTCTTGAGTGGACATT 1998  
 GAGTATTCTTTTACCACCTACAAGACCAGGAGGCATGGTGTCAATTCTCCATTGGGGTATTTATATGAGGTAGAGGTTTCAG 2077  
 GAATCGACAGTAGCTGTGTGGGCTTAGTTTAAAGGACTGAAAGCATAGGGGACTGGTAGACAGTTTCATAGGAAACTGCGG 2156  
 GGAAGGAATGGATACCTTTAAAGACAGTTTGTGGATGCAGATGCTGCCACCCATCATTGAGCACCCCTTGTGTCTCTGGC 2235  
 TTCCTGTCACTGGATCCAGTACCCCTCCATGCTTGGGTCCTTGT TTTACATAAGACAACAAAGCACAAATGTCTGCTGTT 2314  
 TACAATCAAGACGACTACATGGTCCAAACATTTCTTCTCTCTTCTATCACTTGTGGCTTTAACTTCCATTTCCTCCGTT 2393  
 CCTTTT TAAAAATCAAGAAGCACAGTCAGAGCTGCCCCCTGGGATTGCATCAGGGAACGGCTGATCAAGGCATT CAGTGTC 2472  
 CATGACTAAATCTTATCTTTTGTAGCAAATCCTTTTAAAGAACTGAACAATTGCTAAGGCTCAGCAATTTTATACTC 2551  
 CAATGTCTGTGTAAGGTAAATTTTGT TTTGCCATTGAGCCACATTTGGAATTCCTTCTGACGTCAACACTGACAATGCCT 2630  
 ATGGAAATTGCACTTCTGGGTATATGTCCCAGCATCCTTGT TTTCTTATGTTTGGTGAGTAAGGCTCACCCCTTCCAGC 2709  
 AGCTCTACTTCTGTGTGCTGAGGTCCTGTAGAGCCGGGGCTTGGGCACAGACATGAGGCAGACTTGTGCATGCTCTTTC 2788  
 TTGGCAACACTTGGCTCATATTTCTTGT TCTCTTTTGATAGAGTCCTGTTTCTTATGTATTTAAAAAATAATAAAAGTG 2867  
 AATTTAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 2915

Fig. 4D

	10	20	30	40	50	60	70
Hum.	MRRQPAKVAALLLGLLLECTEAKKHCWYFEGLYPTYYICRSYEDCCGSRCCVRLSIQRLWYFWFLMMG						
Mur.	MGRRLGRVAALLLGLLVECTEAKKHCWYFEGLYPTYYICRSYEDCCGSRCCVRLSIQRLWYFWFLMMG						
	10	20	30	40	50	60	70
Hum.	80	90	100	110	120	130	140
	VLFCGAGFFIRRRMYPPPLIEEPAFNVSYTRQPPNPGPGAQQPGPPYYTDPGGPGMNPVGNSMAMAFQV						
Mur.	VLFCGAGFFIRRRMYPPPLIEEPTFNVSYTRQPPNPAPGAQQMGPPYYTDPGGPGMNPVGNTMAMAFQV						
	80	90	100	110	120	130	140
Hum.	150	160	170				
	PPNSPQGSVACPPPPAYCNTPPPPYEQVVAK						
Mur.	QPNSPFGGTTYPPPPSYCNTPPPPYEQVVKDK						
	150	160	170				

Fig. 4F

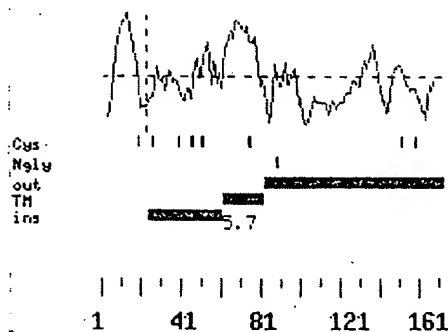


Fig. 4G

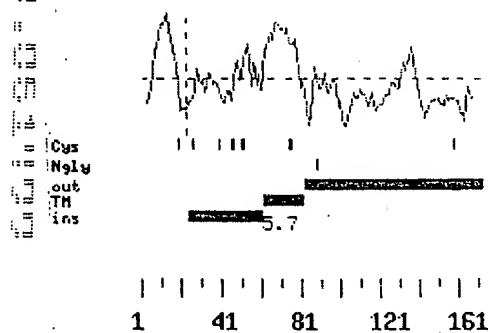


Fig. 5A

GTCGACCCACGCGTCCGCAGCTTTGGACACTTCCTCTGCTTGAGGACACCTTGACTAACCTCCAAGGGCAACTAAAGGA																			79						
																M	C	T	K	T	I				6
TCAAGAAAGGCCCAGCACAGCAGAAGATCAGCTGGATCTAGCTCCTGCAGGAG ATG TGT ACA AAG ACA ATC																			150						
P	V	L	W	G	C	F	L	L	W	N	L	Y	V	S	S	S	Q	T	I	26					
CCA	GTC	CTC	TGG	GGA	TGT	TTC	CTC	CTG	TGG	AAT	CTC	TAT	GTC	TCA	TCC	TCT	CAG	ACC	ATT	210					
Y	P	G	I	K	A	R	I	T	Q	R	A	L	D	Y	G	V	Q	A	G	46					
TAC	CCT	GGA	ATC	AAG	GCA	AGG	ATT	ACT	CAG	AGG	GCA	CTT	GAC	TAT	GGT	GTT	CAA	GCT	GGA	270					
M	K	M	I	E	Q	M	L	K	E	K	K	L	P	D	L	S	G	S	E	66					
ATG	AAG	ATG	ATT	GAG	CAA	ATG	CTA	AAA	GAA	AAG	AAA	CTC	CCA	GAT	TTA	AGC	GGT	TCT	GAG	330					
S	L	E	F	L	K	V	D	Y	V	N	Y	N	F	S	N	I	K	I	S	86					
TCT	CTT	GAA	TTT	CTA	AAA	GTT	GAT	TAT	GTA	AAC	TAC	AAT	TTT	TCA	AAT	ATA	AAA	ATC	AGT	390					
A	F	S	F	P	N	T	S	L	A	F	V	P	G	V	G	I	K	A	L	106					
GCC	TTT	TCA	TTT	CCA	AAT	ACC	TCA	TTG	GCT	TTT	GTG	CCT	GGA	GTG	GGA	ATC	AAA	GCG	CTA	450					
T	N	H	G	T	A	N	I	S	T	D	W	G	F	E	S	P	L	F	V	126					
ACC	AAC	CAT	GGC	ACT	GCC	AAC	ATC	AGC	ACA	GAC	TGG	GGG	TTC	GAG	TCT	CCA	CTT	TTT	GTT	510					
L	Y	N	S	F	A	E	P	M	E	K	P	I	L	K	N	L	N	E	M	146					
CTG	TAT	AAC	TCC	TTT	GCT	GAG	CCC	ATG	GAG	AAA	CCC	ATT	TTA	AAG	AAC	TTA	AAT	GAA	ATG	570					
L	C	P	I	I	A	S	E	V	K	A	L	N	A	N	L	S	T	L	E	166					
CTC	TGT	CCC	ATT	ATT	GCA	AGT	GAA	GTC	AAA	GCG	CTA	AAT	GCC	AAC	CTC	AGC	ACA	CTG	GAG	630					
V	L	T	K	I	D	N	Y	T	L	L	D	Y	S	L	I	S	S	P	E	186					
GTT	TTA	ACC	AAG	ATT	GAC	AAC	TAC	ACT	CTG	CTG	GAT	TAC	TCC	CTA	ATC	AGT	TCT	CCA	GAA	690					
I	T	E	N	Y	L	D	L	N	L	K	G	V	F	Y	P	L	E	N	L	206					
ATT	ACT	GAG	AAC	TAC	CTT	GAC	CTG	AAC	TTG	AAG	GGT	GTA	TTT	TAC	CCA	CTG	GAA	AAC	CTC	750					
T	D	P	P	F	S	P	V	P	F	V	L	P	E	R	S	N	S	M	L	226					
ACC	GAC	CCC	CCC	TTC	TCA	CCA	GTT	CCT	TTT	GTG	CTC	CCA	GAA	CGC	AGC	AAC	TCC	ATG	CTC	810					
Y	I	G	I	A	E	Y	F	F	K	S	A	S	F	A	H	F	T	A	G	246					
TAC	ATT	GGA	ATC	GCC	GAG	TAT	TTC	TTT	AAA	TCT	GCG	TCC	TTT	GCT	CAT	TTC	ACA	GCT	GGG	870					
V	F	N	L	T	L	S	T	E	E	I	S	N	H	F	V	Q	N	S	Q	266					
GTT	TTC	AAT	CTC	ACT	CTC	TCC	ACC	GAA	GAG	ATT	TCC	AAC	CAT	TTT	GTT	CAA	AAC	TCT	CAA	930					
G	L	G	N	V	L	S	R	I	A	E	I	Y	I	L	S	Q	P	F	M	286					
GGC	CTT	GGC	AAC	GTG	CTC	TCC	CGG	ATT	GCA	GAG	ATC	TAC	ATC	TTG	TCC	CAG	CCC	TTC	ATG	990					
V	R	I	M	A	T	E	P	P	I	I	N	L	Q	P	G	N	F	T	L	306					
GTG	AGG	ATC	ATG	GCC	ACA	GAG	CCT	CCC	ATA	ATC	AAT	CTA	CAA	CCA	GGC	AAT	TTC	ACC	CTG	1050					
D	I	P	A	S	I	M	M	L	T	Q	P	K	N	S	T	V	E	T	I	326					



GTT TCC ATG GAC TTC GTT GCT AGT ACC AGT GTT GGC CTG GTT ATT TTG GGA CAA AGA CTG	1170
V C S L S L N R F R L A L P E S N R S N	366
GTC TGC TCC TTG TCT CTG AAC AGA TTC CGC CTT GCT TTG CCA GAG TCC AAT CGC AGC AAC	1230
I E V L R F E N I L S S I L H F G V L P	386
ATT GAG GTC TTG AGG TTT GAA AAT ATT CTA TCG TCC ATT CTT CAC TTT GGA GTC CTC CCA	1290
L A N A K L Q Q G F P L P N P H K F L F	406
CTG GCC AAT GCA AAA TTG CAG CAA GGA TTT CCT CTG CCC AAT CCA CAC AAA TTC TTA TTC	1350
V N S D I E V L E G F L L I S T D L K Y	426
GTC AAT TCA GAT ATT GAA GTT CTT GAG GGT TTC CTT TTG ATT TCC ACC GAC CTG AAG TAT	1410
E T S S K Q Q P S F H V W E G L N L I S	446
GAA ACA TCC TCA AAG CAG CAG CCA AGT TTC CAC GTA TGG GAA GGT CTG AAC CTG ATA AGC	1470
R Q W R G K S A P *	456
AGA CAG TGG AGG GGG AAG TCA GCC CCT TGA	1500
TTGCCGGTTTGTCAATTTCACCCCAGGAAGTAAATGGTCCTTAATCCTACAACCTACTGTAAACCCAGAAGGGAAAGACAGT	1579
AGACACTGGAATTGTAAAGCCCTTGTGAATTGCTTAGGCAGAAAAGTTTCTTTCTTAAGCCTTCAGGAACCCAGAATAA	1658
GGCAGACTCTGTAAAGGGATAAATAGAGGTGTCTGAATGTGAGTGTATGCATGCTGCGTGTGTCTGTGTTTATGTTTG	1737
TTTGTGTTTGGGGCAAGAAAGATTCTAGGACAAGAGCTAGGCATGTACTTCTGACCAGGTGGGTAAGCAACTCTAAG	1816
TCTGTATTTGTATTGGTCATTCTCAGTGGAAATCCCTTAGGCCCTCTAGTGGTTTTCCCTACCTGCATATTGGTTTTTC	1895
ATGTTTTATATTCACTGTTACTATCTTCTGTGTTTAATTAAATTTGTTTTCTATCAAAAAAAAAAAAAAAAAAAGGGC	1974
GGCCGC	1980

Fig. 5B



Fig. 5D

286 10 20 30 40 50 60  
 MCTKT-IPVLWGCFL-LWNLYVSSSQTIYPGIKARITQRALDYGVOAGMKMIEQMLKEKKLPDLGSESL  
 BPI 10 20 30 40 50 60  
 MARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS--DSF  
 70 80 90 100 110 120 130  
 286 EFLKVDYVNYNFSNIKISAFSFPNTSLAFVPGVGIKALTNHGTANISTDWGFESPLFVLYNSFAEPME--  
 BPI 70 80 90 100 110 120 130  
 KIKHLGKGHYSFYSDIREFQLPSSQISMVNVGLKFSISNANIKISGKWKAKRFLKMSGNFDLSIEGM  
 140 150  
 286 -----KPI-----LKN-LNEMLCPIIASE  
 BPI 140 150 160 170 180 190 200  
 SISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKSKVGMILQLFHKKIESALRNKMNSQVCEKVTNS  
 160 170 180 190 200 210 220  
 286 VKA-LNANLSTLEVLTKIDNYTLTDYSLISSPEITENYLDLNLKGVFYPLENLTDPFSPVPFVLPERSN  
 BPI 160 170 180 190 200 210 220  
 VSSKLQPYFQTLPMVKIDSVAGINYGLVAPPATTAETLDVQMKGEFYSENHNPPPFAPPVMEFPAHD  
 230 240 250 260 270 280 290  
 286 SMLYIGIAEYFFKSASFHFTAGVFNLTSTEEISNH--FVQNSQGLGNVLSRIAETIYILSQPFMVRIMA  
 BPI 230 240 250 260 270 280 290  
 RMVYLGLSDYFFNTAGLVYQEAQVGLKMTLRDDMIPKESKFRLLTKFFGTFLPEVAKKFP-NMKIQIHVSA  
 300 310 320 330 340 350 360  
 286 TEPPIIINLQPGNFTLDIPASIMMLTQPKNSTVETIVSMDFVASTSVGLVILGQRLVCSLSLNRFRALPE  
 BPI 300 310 320 330 340 350 360  
 STPPHLSVQPTGLTFYPAVDVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELKH  
 370 380 390 400 410 420 430  
 286 SNRSNIEVLRFENILSSILHFGVLPLANAKLQQGFPLPNPHKFLFVNSDIEVLEGFLLISTDLKYETSSK  
 BPI 370 380 390 400 410 420 430  
 SNIGPFPVELLQDIMNYIVPILVLRVNEKLQKGFPLPTPARVQLYNVVLQPHQNFLLFGADVYK-----  
 440 450  
 286 QQPSFHVWEGLNLISRQWRGKSAP -  
 -----

Fig. 5E

10 20 30 40 50 60  
 286 MCTKTIPVLWGCFLLNLYVSSSQTI--YPGIKARITQRALDYGVQAGMKMIEQMLKEKKLPDLSGSESL  
 RENP MGALARAL--PSILLALLLTSTPEALGANPGLVARITDKGLQYAAQEGLLALQSELLRITLPDFTG--DL  
 10 20 30 40 50 60  
 70 80 90 100 110 120 130  
 286 EFLKVDYVNYNFSNIKISAFSFPNTSLAFVPGVGIKALTNHGTANISTDWGFESPLFVLYNSFAEPME--  
 RENP RIPHVGRGRYEFHSLNIHEFQLPSSQISMVPNVGLKFSISNANIKISGKWKAKRFLKMSGNFDLSEIGM  
 70 80 90 100 110 120 130  
 140 150  
 286 -----KPI-----LKN-LNEMLCPIIASE  
 RENP SISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSKVGVLIQLFHKKIESALRNKMNSQVCEKVTNS  
 140 150 160 170 180 190 200  
 160 170 180 190 200 210 220  
 286 VKA-LNANLSTLEVLTKIDNYTLDDYSLISSPEITENYLDLNLKGVFYPLENLTDPPFSPVPFVLPERSN  
 RENP VSSKLQPYFQTLFVMTKIDSVAGINYGLVAPPATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHD  
 210 220 230 240 250 260 270  
 230 240 250 260 270 280 290  
 286 SMLYIGIAEYFFKSASFHFTAGVFNLTSTEEISNH--FVQNSOQLGNVLSRIAIEIYILSQPFMVRIMA  
 RENP RMVYLGLSDYFFNTAGLVYQEAGVLKMTLRDDMIPKESKFRLLTKFFGTFLPEVAKKFP-NMKIQIHVSA  
 280 290 300 310 320 330 340  
 300 310 320 330 340 350 360  
 286 TEPPPIINLQPGNFTLDIPASIMMLTQPKNSTVETIVSMDFVASTSVGLVILGQRLVCSSLNRFRALALPE  
 RENP STPHLSVQPTGLTFYPAVDVQALAVLPNSSLASFLIGMHTTGSMEVSAESNRLVGELKLDRLLELKH  
 350 360 370 380 390 400 410  
 370 380 390 400 410 420 430  
 286 SNRSNIEVLRFENILSSILHFGVLPANAKLQOGFPLPNPHKFLFVNSDIEVLEGFLLISTDLKYETSSK  
 RENP SNIGFPFVELLQDIMNYIVPILVLPVNEKLQKGFPLPTPARVQLYNVVLQPHQNFLLFGADVYK----  
 420 430 440 450 460 470 480  
 440 450  
 286 QQPSFHVWEGNLNISRQWRGKSAP -

Fig. 6A

GTCGACCCACGCGTCCGGGGAATTGCAGCAGGAAAAATATGTGAAGAGTTTTTAAACCCACAAATTCTTCTTACTTTAGA 79

ATTAGTTGTTACATTGGCAGGAAAAAATAAATGCAGATGTTGGACC M L E T L S R Q 8  
 ATG TTG GAA ACC TTG TCA AGA CAG 149

W I V S H R M E M W L L I L V A Y M F Q 28  
 TGG ATT GTC TCA CAC AGA ATG GAA ATG TGG CTT CTG ATT CTG GTG GCG TAT ATG TTC CAG 209

R N V N S V H M P T K A V D P E A F M N 48  
 AGA AAT GTG AAT TCA GTA CAT ATG CCA ACT AAA GCT GTG GAC CCA GAA GCA TTC ATG AAT 269

I S E I I Q H Q G Y P C E E Y E V A T E 68  
 ATT AGT GAA ATC ATC CAA CAT CAA GGC TAT CCC TGT GAG GAA TAT GAA GTC GCA ACT GAA 329

D G Y I L S V N R I P R G L V Q P K K T 88  
 GAT GGG TAT ATC CTT TCT GTT AAC AGG ATT CCT CGA GGC CTA GTG CAA CCT AAG AAG ACA 389

G S R P V V L L Q H G L V G G A S N W I 108  
 GGT TCC AGG CCT GTG GTG TTA CTG CAG CAT GGC CTA GTT GGA GGT GCT AGC AAC TGG ATT 449

S N L P N N S L G F I L A D A G F D V W 128  
 TGC AAC CTG CCC AAC AAT AGC CTG GGC TTC ATT CTG GCA GAT GCT GGT TTT GAC GTG TGG 509

M G N S R G N A W S R K H K T L S I D Q 148  
 ATG GGG AAC AGC AGG GGA AAC GCC TGG TCT CGA AAA CAC AAG ACA CTC TCC ATA GAC CAA 569

D E F W A F S Y D E M A R F D L P A V I 168  
 GAT GAG TTC TGG GCT TTC AGT TAT GAT GAG ATG GCT AGG TTT GAC CTT CCT GCA GTG ATA 629

N F I L Q K T G Q E K I Y Y V G Y S Q G 188  
 AAC TTT ATT TTG CAG AAA ACG GGC CAG GAA AAG ATC TAT TAT GTC GGC TAT TCA CAG GGC 689

T M G F I A F S T M P E L A Q K I K M 208  
 ACC ACC ATG GGC TTT ATT GCA TTT TCC ACC ATG CCA GAG CTG GCT CAG AAA ATC AAA ATG 749

Y F A L A P I A T V K H A K S P G T K F 228  
 TAT TTT GCT TTA GCA CCC ATA GCC ACT GTT AAG CAT GCA AAA AGC CCC GGG ACC AAA TTT 809

L L L P D M M I K G L F G K K E F L Y Q 248  
 TTG TTG CTG CCA GAT ATG ATG ATC AAG GGA TTG TTT GGC AAA AAA GAA TTT CTG TAT CAG 869

T R F L R Q L V I Y L C G Q V I L D Q I 268  
 ACC AGA TTT CTC AGA CAA CTT GTT ATT TAC CTT TGT GGC CAG GTG ATT CTT GAT CAG ATT 929

C S N I M L L L G G F N T N N M N M S R 288  
 TGT AGT AAT ATC ATG TTA CTT CTG GGT GGA TTC AAC ACC AAC AAT ATG AAC ATG AGC CGA 989

A S V Y A A H T L A G T S V Q N I L H W 308  
 GCA AGT GTA TAT GCT GCC CAC ACT CTT GCT GGA ACA TCT GTG CAA AAT ATT CTA CAC TGG 1049

S Q A V N S G E L R A F D W G S E T K N 328  
 AGC CAG GCA GTG AAT TCT GGT GAA CTC CGG GCA TTT GAC TGG GGG AGT GAG ACC AAA AAT 1109

L E K C N Q P T P V R Y R V R D M T V P 348

CTG GAA AAA TGC AAT CAG CCA ACT CCT GTA AGG TAC AGA GTC AGA GAT ATG ACG GTC CCT	1169
T A M W T G G Q D W L S N P E D V K M L	368
ACA GCA ATG TGG ACA GGA GGT CAG GAC TGG CTT TCA AAT CCA GAA GAC GTG AAA ATG CTG	1229
L S E V T N L I Y H K N I P E W A H V D	388
CTC TCT GAG GTG ACC AAC CTC ATC TAC CAT AAG AAT ATT CCT GAA TGG GCT CAC GTG GAT	1289
F I W G L D A P H R M Y N E I I H L M Q	408
TTC ATC TGG GGT TTG GAT GCT CCT CAC CGT ATG TAC AAT GAA ATC ATC CAT CTG ATG CAG	1349
Q E E T N L S Q G R C E A V L *	424
CAG GAG GAG ACC AAC CTT TCC CAG GGA CGG TGT GAG GCC GTA TTG TGA	1397
AGCATCTGACACTGACGATCTTAGGACAACCTCCTGAGGGATGGGGCTAGGACCCATGAAGGCAGAATTACGGAGAGCA	1476
GAGACCTAGTATACATTTTTTCAGATTCCCTGCACTTGGCACTAAATCCGACACTTACATTTACATTTTTTTTTCTGTAAA	1555
TTAAAGTACTTATTAGGTAAATAGAGGTTTTGTATGCTATTATATATTCTACCATCTTGAAGGGTAGGTTTTACCTGAT	1634
AGCCAGAAAAATATCTAGACATTCTCTATATCATTCAGGTAAATCTCTTTAAAAACACCTATTGTTTTTTCTATAAGCCAT	1713
ATTTTTGGAGCACTAAAGTAAAAATGGCAAATTTGGGACAGATATTGAGGTCTGGAGTCTGTGGATTATTGTTGACTTTGA	1792
CAAAATAAGCTAGACATTTTCACCTTGTTGCCACAGAGACATAACACTACCTCAGGAAGCTGAGCTGCTTTAAGGACAA	1871
CAACAACAAAATCAGTGTTACAGTATGGATGAAATCTATGTTAAGCATTCTCAGAATAAGGCCAAGTTTTATAGTTGCA	1950
TCTCAGGGAAGAAAATTTTATAGGATGTTTATGAGTTCTCCAATAAATGCATTCTGCATTACATAAAAAAAAAAAAAAA	2029
AAAAAGGGCGGCCGC	2044

Fig. 6B

Fig. 6C

```

294 10      20      30      40      50      60      70
HLP M-----WLL---LTMASLISVLGTTGHLFGKLH-----PGSPEVTMNISQMITYWGYPNEEYEVVTEG
      10      20      30      40      50

294 80      90      100     110     120     130     140
HLP YILSVNRIPRGLVQPKKTGSRPVVLLQHGLVGGASNWISNLPNNSLGFIADAGFDVWMGNSRGNAWSRK
      60      70      80      90      100     110     120
YILEVNRIPYGKKNSGNTGQRPVFLQHGLLASATNWNISNLPNNSLAFILADAGYDVWLGNSRGNTWARR

294 150     160     170     180     190     200     210
HLP HKTLSIDQDEFWAFSYDEMARFDLPAVINFILOKQTGQEKIYYVGYSQGTMTMGFIAFSTMPELAQKIKMYF
      130     140     150     160     170     180     190
NLYYSPDSVEFWAFSFDDEMAKYDLPATIDFIVKKTGQKQLHYVGHSGGTTIGFIAFSTNPSLAKRIKTFY

294 220     230     240     250     260     270
HLP ALAPIATVKHAKSPGKTFLLLPDMMIKGLFGKKEFLYQTRFLRQ-LVIYLCGQVILDQICSNIMLLLGGF
      200     210     220     230     240     250     260
ALAPVATVKYTKSLINKLRFVPQSLFKFIFGDKIF-YPHNFFDQFLATEVCSREMLNLLCSNALFIICGF

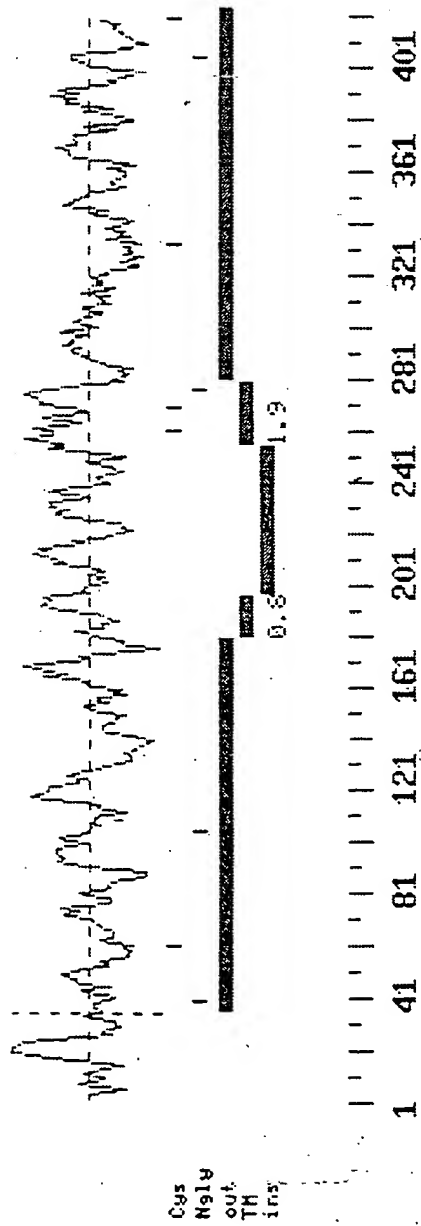
294 280     290     300     310     320     330     340
HLP NTNNMNMMSRASVYAAHTLAGTSVQNILHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRYRVRDMTVPT
      270     280     290     300     310     320     330
DSKNFNTSRLDVYLSHNPAGTSVQNMFWHTQAVKSGKFQAYDWGSPVQNRMHYDQSQPPYYNVTAMNVPI

294 350     360     370     380     390     400     410
HLP AMWTGGQDWLSNPEDVKMLLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNEIIHLMQQEETNLSQGRC
      340     350     360     370     380     390
AVWNGGKDLLADPQDVGLLLPKLPNLIYHKEIPFYNHLDFIWAMDAPQEVYNDIVSMISEDKK-----

294 420
HLP EAVL
HLP -----

```

Fig. 6D





```

10      20      30      40      50      60
294 MLETLSRQWIVSHRMEMWLLILVAYMFQRNVNSVHMPK--AVDPEAFMNISEIIQHOGYPCEEYEVATE
:      :      :      :      :      :      :      :      :      :      :      :      :
LAL M-----KMRFLGLVVCLVLWPLHSEGSGGKLTAVDPETNMNVSEIISYWGFPSSEYLVETE
      10      20      30      40      50

70      80      90      100      110      120      130
294 DGYILSVNRIPRGLVQPKKTGSRPVVLLQHGLVGGASNWISNLPNNSLGFILADAGFDVWVGNSRGNWS
:      :      :      :      :      :      :      :      :      :      :      :
LAL DGYILCLNRI PHGRKNHSDKGPKPVVFLQHGLLADSSNWVTNLANSSLGFILADAGFDVWVGNSRGNTWS
      60      70      80      90      100      110      120

140      150      160      170      180      190      200
94 RKHKTL SIDQDEFWAFSYDEMARFDLPAVINFILQKTGQEKIYYVGYSQGTTMGFIAFSTMPELAQKIKM
:      :      :      :      :      :      :      :      :      :      :      :
LAL RKHKTL SVSQDEFWAFSYDEMAKYDLPASINFILNKTGQEQVYYVGHSQGTITIGFIAFSQIPELAKRIKM
      130      140      150      160      170      180      190

210      220      230      240      250      260      270
294 YFALAPIATVKHAKSPGTKFLLLPDMMIKGLFGKKEFLYQTRFLRQLVIYLCGQVILDQICSNIMLLLG
:      :      :      :      :      :      :      :      :      :      :      :
LAL FFALGPVASVAFCTSPMAKLGRLPDHLIKDLFGDKEFLPQSAFLKWLGTHVCTHVILKELCGNLCFLLCG
      200      210      220      230      240      250      260

280      290      300      310      320      330      340
294 FNTNNMNSRASVYAAHTLAGTSVQNILHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRYRVRDMTVP
:      :      :      :      :      :      :      :      :      :      :      :
LAL FNERNLNMSRVDVYTTHTSPAGTSVQNMHLWSQAVKFQKFAFDWGSSAKNYFHYNQSYPTYNVKDMLVP
      270      280      290      300      310      320      330

350      360      370      380      390      400      410
294 TAMWTGGQDWLSNPEDVKMLLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNEIIHLMQOEETNLSQGR
:      :      :      :      :      :      :      :      :      :      :      :
LAL TAVWSGGHDWLADVVDVNILLTQITNLV FHESIPEWEHLDFIWGLDAPWRLYNKIINLMRKYQ-----
      340      350      360      370      380      390

420
294 CEAVL
LAL -----

```

Fig. 7A

GTCGACCCACGCGTCCACGGCGAGGGCTCCCGGGGCGCAGCATTGCCCCCCTGCACCACCTCACCAAG																			M A	2
ATG GCT																				75
T	L	G	H	T	F	P	F	Y	A	G	P	K	P	T	F	P	M	D	T	22
ACT	TTG	GGA	CAC	ACA	TTC	CCC	TTC	TAT	GCT	GGC	CCC	AAG	CCA	ACC	TTC	CCG	ATG	GAC	ACC	135
T	L	A	S	I	I	M	I	F	L	T	A	L	A	T	F	I	V	I	L	42
ACT	TTG	GCC	AGC	ATC	ATC	ATG	ATC	TTT	CTG	ACT	GCA	CTG	GCC	ACG	TTC	ATC	GTC	ATC	CTG	195
P	G	I	R	G	K	T	R	L	F	W	L	L	R	V	V	T	S	L	F	62
CCT	GGC	ATT	CGG	GGA	AAG	ACG	AGG	CTG	TTC	TGG	CTG	CTT	CGG	GTG	GTG	ACC	AGC	TTA	TTC	255
I	G	A	A	I	L	A	V	N	F	S	S	E	W	S	V	G	Q	V	S	82
ATC	GGG	GCT	GCA	ATC	CTG	GCT	GTG	AAT	TTC	AGT	TCT	GAG	TGG	TCT	GTG	GGC	CAG	GTC	AGC	315
T	N	T	S	Y	K	A	F	S	S	E	W	I	S	A	D	I	G	L	Q	102
ACC	AAC	ACA	TCA	TAC	AAG	GCC	TTC	AGT	TCT	GAG	TGG	ATC	AGC	GCT	GAT	ATT	GGG	CTG	CAG	375
V	G	L	G	G	V	N	I	T	L	T	G	T	P	V	Q	Q	L	N	E	122
GTC	GGG	CTG	GGT	GGA	GTC	AAC	ATC	ACA	CTC	ACA	GGG	ACC	CCC	GTG	CAG	CAG	CTG	AAT	GAG	435
T	I	N	Y	N	E	E	F	T	W	R	L	G	E	N	Y	A	E	E	C	142
ACC	ATC	AAT	TAC	AAC	GAG	GAG	TTC	ACC	TGG	CGC	CTG	GGT	GAG	AAC	TAT	GCT	GAG	GAG	TGT	495
A	K	A	L	E	K	G	L	P	D	P	V	L	Y	L	A	E	K	F	T	162
GCA	AAG	GCT	CTG	GAG	AAG	GGG	CTG	CCA	GAC	CCT	GTG	TTG	TAC	CTA	GCT	GAG	AAG	TTC	ACT	555
P	R	S	P	C	G	L	Y	R	Q	Y	R	L	A	G	H	Y	T	S	A	182
CCA	AGA	AGC	CCA	TGT	GGC	CTA	TAC	CGC	CAG	TAC	CGC	CTG	GCG	GGA	CAC	TAC	ACC	TCA	GCC	615
M	L	W	V	A	F	L	C	W	L	L	A	N	V	M	L	S	M	P	V	202
ATG	CTA	TGG	GTG	GCA	TTC	CTC	TGC	TGG	CTG	CTG	GCC	AAT	GTG	ATG	CTC	TCC	ATG	CCT	GTG	675
L	V	Y	G	G	Y	M	L	L	A	T	G	I	F	Q	L	L	A	L	L	222
CTG	GTA	TAT	GGT	GGC	TAC	ATG	CTA	TTG	GCC	ACG	GGC	ATC	TTC	CAG	CTG	TTG	GCT	CTG	CTC	735
F	F	S	M	A	T	S	L	T	S	P	C	P	L	H	L	G	A	S	V	242
TTC	TTC	TCC	ATG	GCC	ACA	TCA	CTC	ACC	TCA	CCC	TGT	CCC	CTG	CAC	CTG	GGC	GCT	TCT	GTG	795
L	H	T	H	H	G	P	A	F	W	I	T	L	T	T	G	L	L	C	V	262
CTG	CAT	ACT	CAC	CAT	GGG	CCT	GCC	TTC	TGG	ATC	ACA	TTG	ACC	ACA	GGA	CTG	CTG	TGT	GTG	855
L	L	G	L	A	M	A	V	A	H	R	M	Q	P	H	R	L	K	A	F	282
CTG	CTG	GGC	CTG	GCT	ATG	GCG	GTG	GCC	CAC	AGG	ATG	CAG	CCT	CAC	AGG	CTG	AAG	GCT	TTC	915
F	N	Q	S	V	D	E	D	P	M	L	E	W	S	P	E	E	G	G	L	302
TTC	AAC	CAG	AGT	GTG	GAT	GAA	GAC	CCC	ATG	CTG	GAG	TGG	AGT	CCT	GAG	GAA	GGT	GGA	CTC	975
L	S	P	R	Y	R	S	M	A	D	S	P	K	S	Q	D	I	P	L	S	322
CTG	AGC	CCC	CGC	TAC	CGG	TCC	ATG	GCT	GAC	AGT	CCC	AAG	TCC	CAG	GAC	ATT	CCC	CTG	TCA	1035
E	A	S	S	T	K	A	Y	C	K	E	A	H	P	K	D	P	D	C	A	342
GAG	GCT	TCC	TCC	ACC	AAG	GCA	TAC	TGT	AAG	GAG	GCA	CAC	CCC	AAA	GAT	CCT	GAT	TGT	GCT	1095

L *	344
TTA TAA	1101
CATTCTCCCCGTGGAGGCCACCTGGACTTCCAGTCTGGCTCCAAACCTCATTGGCGCCCCATAAAACCAGCAGAACTG	1180
CCCTCAGGGTGGCTGTTACCAGACACCCAGCACCAATCTACAGACGGAGTAGAAAAAGGAGGCTCTATATACTGATGTT	1259
AAAAAACAAAACAAAACAAAAGCCCTAAGGGACTGAAGAGATGCTGGGCCTGTCCATAAAGCCTGTTGCCATGATAAG	1338
GCCAAGCAGGGGCTAGCTTATCTGCACAGCAACCCAGCCTTTCCGTGCTGCCTTGCCTCTTCAAGATGCTATTCACTGA	1417
AACCTAACTTCACCCCCATAACACCAGCAGGGTGGGGGTACATATGATTCTCCTATGGTTTCCTCTCATCCCTCGGCA	1496
CCTCTTGTTTTCTTTTTCTGGGTTCTTTTTGTTCTTCTTTACTTCTCCAGCTTGTGTGGCCTTTTGGTACAATGAA	1575
AGACAGCACTGGAAAGGAGGGGAAACCAAACCTTCTCATCCTAGGTCTAACATTAACCAACTATGCCACATTCTCTTTGA	1654
GCTTCAGTTCCTCAAATTTGCTACATAAGATTGCAAGACTTGCCAAGAATCTTGGGATTTATCTTTCTATGCCTTGCTGA	1733
CACCTACCTTGGCCCTCAAACACCCACTCACAGAAGCCAGGTGGGAAGTTAGGGAATCAACTCCAAAACGCTATTCTCT	1812
TCCCACCCCACTCAGCTGGGCTAGCTGAGTGGCATCCAGGACGGGGGAGTGGGTGACCTGCCTCATCACTGCCACCTAA	1891
CGTCCCCCTGGGGTGGTTTCAGAAAGATGCTAGCTCTGGTAGGGTCCCTCCGGCCTCACTAGAGGGCGCCCTATTACTC	1970
TGGAGTCGACGCAGAGAATCAGGTTTCACAGCACTGCGGAGAGTGTACTAGGCTGTCTCCAGCCCAGCGAAGCTCATGA	2049
GGACGTGCGACCCCGGCGCGGAGAAGCCATGAAAATTAATGGGAAAAACAGTTTTTAAAAAAAAAAAAAAAAAAGGGCG	2128
GCCGC	2133

Fig. 7B

Fig. 7C

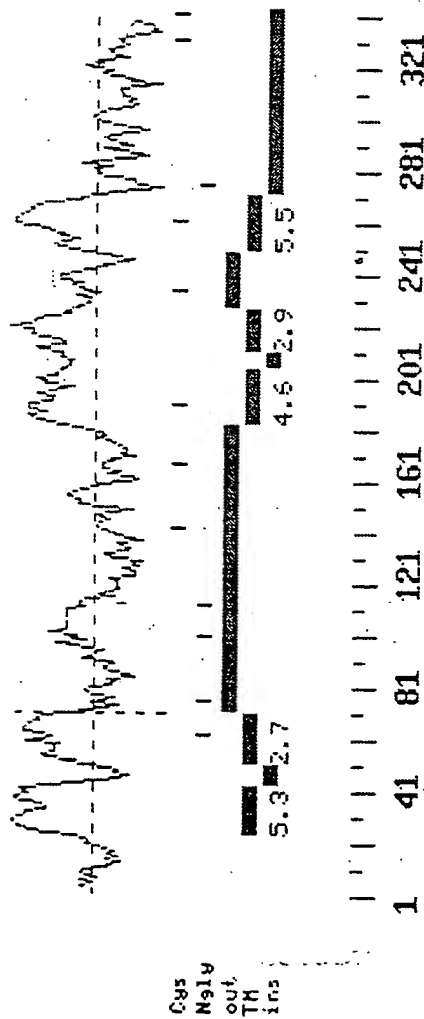


Fig. 7D

	10	20	30	40	50	60	70
296	MATLGHTFPFYAGPKPTFPMDDTLASIIIMIFLTALATFIVILPGIRGKTRLFWLLRVVTSLSFIGAAILAV						
	:	...	:	:	:	:	:
CRP	M-RIAH-----ASSRGNI-----SIFSVFLIPLIAYILILPGVR-RKRVVTTVTYVLMMLAVGGALIAS						
	10	20	30	40	50		

	80	90	100	110	120	130
296	NFSSEWSVGQVSTNTSYKAFSSEWISADIGLQVGLGGVNITL-----TGTPVQQLNETIN--YNEEFTW					
	:	:	:	:	:	:
CRP	LIYPCWASGSQMIYTQFRGHSNERILAKIGVEIGLQKVNVTLKFERLLSSNDVLPGSDMTELYYNNEGFDI					
	60	70	80	90	100	120

	140	150	160	170	180	190	200
296	RLGENYAECAKALEKGLPDPVLYLAEKFT-PRSPCGLYRQYRLAGHYTSAMLWVAFLCWLLIANV-MLSM						
	:	:	:	:	:	:	:
CRP	SGISSMAEALHHGLENGLPYPMLSVLEYFSLNQDSFDWGRHYRVAGHYTHAAIWFAFACWCLSVVLMFL						
	130	140	150	160	170	180	190

	210	220	230	240	250	260
296	PVLVYGGYMLLATGIFQLLALLFFSMATSLTSPCPLHL---GASVLHTHHGPAF---WITLTTGLLCVL					
	:	:	:	:	:	:
CRP	PHNAYKS--ILATGISCLIACLVYL---LLSPCELRIAFRTGENFERVDLTATFSFCFYLFIFAIGILCVL					
	200	210	220	230	240	260

	270	280	290	300	310	320
296	LGLAMAVAHMQPHRLKAFFNQSVDEDPMLEW-----SPEEGGLSPRY--RSMADSPKSQDIPLSEAS					
	:	:	:	:	:	:
CRP	CGLGLGICEHWRIYITLSTFLDASLDEHVGPKWKKLPTGGPALQGVQIGAYGTNTTNSRDKNDISSDKTA					
	270	280	290	300	310	330

	330	340
296	STKAY-----CK-----EAHPKDPD-----CA---L	
	:	:
CRP	GSSGFQSRSTSTCQSSASSASLRSQSSIETVHDEAELERTHVHFLQEPCCSSST	
	340	380